

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 39.3625 Seconds
(without alignments)
163.773 Million cell updates/sec

Title: US-09-055-744A-9
Perfect score: 342
Sequence: 1 RQHSISERILSTYIGRSAB.....VGSPOIVESPALVSGTKE 67

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	334	97.7	116	2 JC4968	rev protein - huma
2	333	97.4	116	1 VKLJH3	trans-regulatory s
3	332	97.1	116	2 S33983	rev protein - huma
4	332	97.1	116	4 S14607	rev protein - synt
5	319	93.3	116	2 T09447	rev protein - huma
6	309	90.4	90	1 VKLJBR	trans-regulatory s
7	299	87.4	118	2 S54382	rev protein - huma
8	298	87.1	117	2 T01666	rev protein - huma
9	291	85.1	116	1 P44001	trans-regulatory s
10	286	83.6	115	1 VKLJND	trans-regulatory s
11	118	34.5	124	1 VKLJSI	trans-regulatory s
12	73	21.3	456	2 T49159	hypothetical prote
13	66.5	19.4	273	2 T46108	hypothetical prote
14	66.5	19.4	13055	2 T16580	hypothetical prote
15	64	18.7	158	2 A70510	hypothetical prote
16	63	18.4	800	2 T00034	SART-1 protein - h
17	60.5	17.7	511	2 A56750	archaia - human
18	60	17.5	147	2 A28942	probable peptide d
19	60	17.5	264	2 A28942	pancreatic elastase
20	60	17.5	772	2 D95858	probable aldehyde
21	59.5	17.4	362	2 S69197	oligo1-lacetyl-carri
22	59	17.3	379	2 A81678	conserved hypochet
23	58.5	17.1	828	1 T35479	probable oxidoredu
24	58.5	17.1	1734	2 A54602	microtubule-associ
25	58.5	17.1	3381	2 T42389	versican precursor
26	58	17.0	219	2 B83299	hypothetical prote
27	58	17.0	284	2 S51294	probable membrane
28	58	17.0	364	2 A34867	arrestin - fruit f
29	58	17.0	393	2 T16046	hypothetical prote

30	58	17.0	428	2 G81362	3-phosphoshikimate
31	58	17.0	428	2 JC5338	3-phosphoshikimate
32	57.5	16.8	1088	1 PIXRPR	inner layer protei
33	57	16.7	133	2 A41768	basic helix-loop-h
34	57	16.7	203	2 A86595	hypothetical prote
35	57	16.7	272	2 A81454	phage protein homo
36	57	16.7	363	2 A55081	arrestin 1 - blueb
37	57	16.7	612	2 S53714	probable dinitrifi
38	57	16.7	778	2 AD0432	aerobic respiratio
39	57	16.7	976	2 S40697	processing endopro
40	57	16.7	1273	2 T34558	hypothetical prote
41	56.5	16.5	109	1 K3HUPM	Ig kappa chain V-I
42	56.5	16.5	111	2 S36263	Ig lambda chain V-I
43	56.5	16.5	129	2 S40325	Ig kappa chain - h
44	56.5	16.5	362	2 T14393	probable oleoyl-la
45	56.5	16.5	439	2 B81997	L-serine ammonia-1

ALIGNMENTS

RESULT 1
JC4968
rev protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C:Accession: JC4968
R:Meggio, F.; D'Agostino, D.M.; Cimnale, V.; Chieco-Bianchi, L.; Pinna, L.A.
Biochem. Biophys. Res. Commun. 226, 547-554, 1996
A:Title: Phosphorylation of HIV-1 rev protein: Implication of protein kinase CK2 and pro
A:Reference number: JC4968; MUID:96400295; PMID:8806671
A:Accession: JC4968
A:Molecule type: protein
A:Residues: 1-116 <MEG>
A:Cross-references: UNIPROT:P04618
C:Comment: This protein is a post-transcriptional activator of the unspliced and singly
C:Genetics:
A:Gene: rev
C:Superfamily: AIDS trans-regulatory splicing protein
C:Keywords: phosphoprotein
F:35-50/Region: arginine-rich
F:8,99,106/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 97.7% Score 334; DB 2; Length 116;
Best Local Similarity 97.0%; Pred. No. 1.3e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQHSISERILSTYIGRSABPVPLQLPELRLTLDNCNDCGTSQGVGSPQIVLSPAV 60
DB 50 RQHSISERILSTYIGRSABPVPLQLPELRLTLDNCNDCGTSQGVGSPQIVLSPAV 109

QY 61 LESGTKE 67
DB 110 LESGTKE 116

RESULT 2
VKLJH3
trans-regulatory splicing protein - human immunodeficiency virus type 1 (isolate HTLV-II
N:Alternate names: anti-repression trans-activator
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (nan)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 23-Feb-1997
C:Accession: A04018
R:Sodroski, J.; Goh, W.C.; Rosen, C.; Dayton, A.; Terwilliger, E.; Haseltine, W.
Nature 321, 412-417, 1986
A:Title: A second post-transcriptional trans-activator gene required for HTLV-III replic
A:Reference number: A04018; MUID:86230863; PMID:3012355
A:Accession: A04018
A:Molecule type: DNA
A:Residues: 1-116 <SOD>
C:Genetics:
A:Gene: trs; art

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S54382
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Accession: S54382
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-118 <THE>
A;Cross-references: UNIPROT:P12483; EMBL:M22639; NID:g329377; PIDN:AAA45364.1; PID:g3293
C;Genetics:
A;Intons: 26/1
C;Superfamily: AIDS trans-regulatory splicing protein

Query Match 87.4%; Score 299; DB 2; Length 118;
Best Local Similarity 86.6%; Pred. No. 2e-28;
Matches 58; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 50 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 109

Qy 61 LESGTKE 67
Db 110 LESGTKE 116

RESULT 8
T01666
rev protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01666
R;Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol
A;Reference number: 214389; MUID:86245056; PMID:2424612
A;Accession: T01666
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-117 <AII>
A;Cross-references: UNIPROT:P04622; EMBL:K03456; NID:g328018; PID:g328020
C;Genetics:
A;Intons: 26/1
C;Superfamily: AIDS trans-regulatory splicing protein

Query Match 87.1%; Score 298; DB 2; Length 117;
Best Local Similarity 86.6%; Pred. No. 2.6e-28;
Matches 58; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 51 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 110

Qy 61 LESGTKE 67
Db 111 LESGTKE 117

RESULT 9
F44001
trans-regulatory splicing protein - human immunodeficiency virus type 1 (strain YU-2)
N;Alternate names: anti-repression trans-activator
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: F44001
R;Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, and biological properties of
A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Accession: F44001
A;Molecule type: DNA

A;Residues: 1-116 <LIY>
A;Cross-references: UNIPROT:P35960; GB:M93258
C;Genetics:
A;Gene: trs; art
A;Intons: 26/1
C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; RNA binding; transcription regulation
F;34-46/Region: arginine-rich RNA-binding pattern

Query Match 85.1%; Score 291; DB 1; Length 116;
Best Local Similarity 85.1%; Pred. No. 1.8e-27;
Matches 57; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 50 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 109

Qy 61 LESGTKE 67
Db 110 LESGTKE 116

RESULT 10
VKLJND
trans-regulatory splicing protein - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: anti-repression trans-activator; art protein; rev protein; trs protei
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 23-Feb-1997
C;Accession: J00072
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immuno
A;Reference number: J00065; MUID:90034200; PMID:2806917
A;Accession: J00072
A;Molecule type: DNA
A;Residues: 1-115 <SEI>
A;Cross-references: GB:M27323
C;Genetics:
A;Gene: rev; trs; art
C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; RNA binding; splicing protein; transcription regulat
F;33-45/Region: arginine-rich RNA-binding pattern

Query Match 83.6%; Score 286; DB 1; Length 115;
Best Local Similarity 82.1%; Pred. No. 6.9e-27;
Matches 55; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 49 ROHSISERILCTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 108

Qy 61 LESGTKE 67
Db 109 LESGTKE 115

RESULT 11
VKLSJI
trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz
N;Alternate names: anti-repression trans-activator; art protein; rev protein; trs protei
C;Species: simian immunodeficiency virus SIVcpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09988
R;Huot, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Main-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUID:90259077; PMID:2168136
A;Accession: S09988
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-124 <HUB>

A:Cross-references: UNIPROT:P17280; EMBL:X52154; NID:G58866; PIDN:CAA36405.1; PID:G76308
C:Genetics:
A:Gene: rev; crs; art
A:Introns: 27/1
C:Superfamily: AIDS trans-regulatory splicing protein
C:Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation

Query Match 34.5%; Score 118; DB 1; Length 124;
Best Local Similarity 46.2%; Pred. No. 8.3e-07;
Matches 24; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OY 1 KQHSISRRISTYIGRSABPVPLQPLPRLTLDCNEDCGTSGTGVSGSQ 52
DB 51 KQISEISGRVATYIGRPPKPDDELPLDKLSLCQCVETDVGTSNTSQPQ 102

RESULT 12

T49159
hypothetical protein T20N10.110 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T49159
R:P:Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; I

submitted to the Protein Sequence Database, April 2000
A:Reference number: 225017
A:Accession: T49159
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-456 <DAN>
A:Cross-references: UNIPROT:Q9LXK5; EMBL:AL353032; GSPDB:GN00061; ATSP:T20N10.110
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone T20N10

A:Gene: ATSP:T20N10.110
A:Map position: 3
A:Introns: 117/3; 142/3; 174/3; 203/2; 243/3; 276/2; 317/1; 345/3; 386/2; 423/3

Query Match 21.3%; Score 73; DB 2; Length 456;
Best Local Similarity 31.1%; Pred. No. 0.82;
Matches 19; Conservative 10; Mismatches 22; Indels 10; Gaps 1;

OY 15 LGRSAEPVPLQPLPRLTLDCNEDCGTSGTGVSGPOLIVESPP-----VLESG 64
DB 13 LGRSSSLAPSRPTDTEDEDDDLAAATAGIDPTIRLMYLANESGDIGINKMLDSG 72

OY 65 T 65
DB 73 T 73

RESULT 13

T46108
hypothetical protein T27B3.10 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C:Accession: T46108
R:Yakutara, G.; Fartmann, B.; Dauner, D.; Steir, W.; Holland, R.; Weichselgartner, M.;

submitted to the Protein Sequence Database, January 2000
A:Reference number: 223022
A:Accession: T46108
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-273 <NVA>
A:Cross-references: UNIPROT:O9M2N8; EMBL:AL137079
C:Genetics:
A:Experimental source: cultivar Columbia; BAC clone T27B3

A:Map position: 3
A:Introns: 47/2; 143/1
A:Note: T27B3.10

Query Match 19.4%; Score 66.5; DB 2; Length 273;
Best Local Similarity 35.7%; Pred. No. 2.8; 23; Indels 9; Gaps 2;
Matches 20; Conservative 4; Mismatches 9; Gaps 2;

OY 1 KQHSISERRI--LSTYIGRSABPVPLQPLPRLTLDCN-----EDCGTSGTGG 47
DB 122 RIITSIGRMGLFLETNIGRDVSVLKFOYERKLNKFTTCGMLSHDAECPTSGNOG 177

RESULT 14

T16580
hypothetical protein K07E12.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T16580
R:Fulton, L.

submitted to the EMBL Data Library, May 1994
A:Description: The sequence of C. elegans cosmid K07E12.
A:Reference number: 218540

A:Accession: T16580
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-13055 <FUL>
A:Cross-references: UNIPROT:Q09165; EMBL:U00054; NID:G485140; PID:G485141; PIDN:AAA50715
A:Experimental source: strain Bristol N2
C:Genetics:

A:Gene: CESP:K07E12.1
A:Introns: 46/3; 85/2; 201/1; 278/2; 470/2; 817/1; 927/1; 960/3; 1265/1; 1322/1; 1478/3;
A:Note: 6014/3; 6159/3; 6665/2; 7266/3; 7895/3; 8669/3; 8726/3; 9803/3; 10937/3; 12234/2; 12298

Query Match 19.4%; Score 66.5; DB 2; Length 13055;
Best Local Similarity 33.9%; Pred. No. 2.1e+02;
Matches 21; Conservative 14; Mismatches 16; Indels 11; Gaps 4;

OY 12 STYIGRSABPVPLQPLPRLTLDCNED-----CGTGTGVSGPOLIVESPAVLESQT 65
DB 611 TTYWL--AAKPPVQVLEPSEWTKESPNDMEIIEC--GAQGVPRKXIMWSGTLIEDGK 665

OY 66 KE 67
DB 666 EE 667

RESULT 15

A70510
hypothetical protein Rv0516c - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: A70510
R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: A70510
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: UNIPROT:Q33361; GB:Z97831; GB:AL123456; NID:G3261825; PIDN:CAB10752.1

A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv0516c

Query Match 18.7%; Score 64; DB 2; Length 158;
Best Local Similarity 34.3%; Pred. No. 3;
Matches 23; Conservative 8; Mismatches 22; Indels 14; Gaps 4;

OY 3 IHSISRRILSTYIGRSABPVPLQPLPRL-----LTIDC--NEPCGTSGTGVSGPOLIV 55
DB 52 VEQISEHVRRPSLG--TNPVTLDELSELSHSGAISLTLIDEDCCRAAGVQWA-----LV 104

OY 56 ESPAVLE 62
DB 105 ASPAVLE 111

Tue Dec 14 17:05:14 2004

us-09-055-744a-9.rpr

Page 5

Search completed: December 14, 2004, 16:43:54
Job time : 40.3625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 212.725 Seconds
(without alignments)
181.220 Million cell updates/sec

Title: US-09-055-744A-9

Perfect score: 342
Sequence: 1 RQHHSISERILSTYLGRSAE.....VGSPQLVSPDAVLESGRKE 67

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	98.8	106	1 REV_HV1B8	P05864 human immun
2	338	98.8	116	1 REV_HV1BR	P04620 human immun
3	338	98.8	116	2 Q72501	Q72501 human immun
4	334	97.7	116	1 REV_HV1H2	P04618 human immun
5	334	97.7	116	2 Q77Y21	Q77Y21 simian-huma
6	334	97.7	116	2 Q77YF8	Q77YF8 human immun
7	334	97.7	116	2 AAB99974	AAB99974 simian-hu
8	334	97.7	116	2 AAD12140	AAD12140 simian-hu
9	334	97.7	116	2 AAC82592	AAC82592 human imm
10	334	97.7	118	1 REV_HV1LW	Q70624 human immun
11	334	97.7	201	1 Q99358	Q99358 human immun
12	333	97.4	116	1 REV_HV1B1	P04616 human immun
13	332	97.1	98	2 Q8Q2T0	Q8Q2T0 human immun
14	332	97.1	107	2 Q8Q2T1	Q8Q2T1 human immun
15	332	97.1	116	1 REV_HV1I2	P04325 human immun
16	332	97.1	116	1 REV_HV1PV	P04617 human immun
17	332	97.1	116	2 Q90176	Q90176 human immun
18	332	97.1	116	2 Q76PP8	Q76PP8 human immun
19	332	97.1	116	2 Q9PXH4	Q9PXH4 human immun
20	332	97.1	116	2 CAAT7626	CAAT7626 human imm
21	330	96.5	116	2 Q6EG60	Q6EG60 human immun
22	329	96.2	116	2 Q72991	Q72991 human immun
23	328	95.9	116	2 Q6YAS9	Q6YAS9 human immun
24	328	95.9	116	2 Q9PXZ1	Q9PXZ1 human immun
25	328	95.9	116	2 AAC040781	AAC040781 human imm
26	327	95.6	116	2 Q74088	Q74088 human immun
27	326	95.3	72	2 Q90641	Q90641 simian-huma
28	326	95.3	116	2 O11406	O11406 simian-huma
29	323	94.4	116	1 REV_HV1S3	P19447 human immun
30	323	94.4	116	2 Q77MH4	Q77MH4 simian-huma
31	323	94.4	116	2 AAG14294	AAG14294 simian-hu

32	319	93.3	116	2 Q75759	Q75759 human immun
33	317	92.7	116	2 Q04146	Q04146 human immun
34	316	92.4	91	2 Q72825	Q72825 human immun
35	316	92.4	91	2 Q72829	Q72829 human immun
36	316	92.4	116	1 REV_HV1UR	P20869 human immun
37	316	92.4	116	2 Q6V357	Q6V357 human immun
38	316	92.4	116	2 Q74597	Q74597 human immun
39	316	92.4	116	2 Q72JF7	Q72JF7 human immun
40	316	92.4	116	2 AAR26415	AAR26415 human imm
41	314	91.8	91	2 Q72779	Q72779 human immun
42	314	91.8	116	2 Q92881	Q92881 human immun
43	314	91.8	119	2 Q8ADT1	Q8ADT1 human immun
44	313	91.5	90	2 Q78232	Q78232 human immun
45	313	91.5	116	2 Q902P9	Q902P9 human immun

ALIGNMENTS

RESULT 1
REV_HV1B8
ID REV_HV1B8 STANDARD: PRT: 106 AA.
AC P05864;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS)
DE (Fragment).
GN Name=REV;
OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11684;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Lyvak K.J., Starcich B.R.,
RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Garbaye J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.",
RL Nature 313:277-284(1985).
CC -!- FUNCTION: Rev appears to act post-transcriptionally to relieve
CC -!- negative repression of Gag and Env production.
CC -!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -!- PTM: Phosphoprotein whose state of phosphorylation is mediated by
CC a specific serine kinase activity present in the nucleus.
CC -----
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CC entities requires a license agreement (see <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, KO2011; AAA44659.1; -
DR PDB; 163D; Model; B=24-40.
DR PDB; 262D; Model; B=24-40.
DR HIV; KO2011; REVSH8.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR006625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW 3D-structure; AIDS; Nuclear protein; Phosphorylation;
KW Transcription regulation.
FT NON TER 1
SQ SEQUENCE 106 AA; 12090 MW; 676F5923829FAD83 CRC64;
Query Match 98.8%; Score 338; DB 1; Length 106;
Best Local Similarity 98.5%; Pred. No. 66-33; Indels 0; Gaps 0;
Matches 66; Conservative 0; Mismatches 1;
1 RQHHSISERILSTYLGRSAEPVQLPLERLTLDNCEDCGTSGTGSGPQLVSPDAVLES

```

Db 40 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 99
Qy 61 LESGTKE 67
Db 100 LESGTKE 106

RESULT 2
REV_HV1B2
ID REV_HV1B2 STANDARD; PRT; 116 AA.
AC P04620;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN Name=REV;
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1), and
OS Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CC NCBI_TaxID=11686, 11698;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=Isolate BRU;
CC BUCKLER C.E., BUCKLER-White A.J., WILLEY R.L., MCCOY J.J.,
CC Submitted (JUN-1988) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Rev appears to act post-transcriptionally to relieve
CC negative repression of Gag and Env production.
CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -1- PTM: Phosphoprotein whose state of phosphorylation is mediated by
CC a specific serine kinase activity present in the nucleus.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: K02013; AAB59746.1; -
CC EMBL: M19821; AAB44986.1; -
CC DR HIV; K02013; REV5BRU.
CC DR HIV; M19821; REV5NL43.
CC DR InterPro: IPR007110; IG-1like.
CC DR InterPro: IPR00625; REV_protein.
CC DR Pfam: PF00424; REV; 1.
CC KM AIDS; Nuclear protein; Phosphorylation; Transcription regulation.
CC VARIANT 11 15 DLKA -> ELIRT (in clone NL-43).
CC VARIANT 21 21 F -> L (in clone NL-43).
CC SEQUENCE 116 AA; 13067 MW; 30DA320AF302FBCD CRC64;

Query Match 98.8%; Score 338; DB 1; Length 116;
Best Local Similarity 98.5%; Pred. No. 6.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 50 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 109
Qy 61 LESGTKE 67
Db 110 LESGTKE 116

RESULT 3

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```

Q72501
ID Q72501 PRELIMINARY; PRT; 116 AA.
AC Q72501;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE REV protein.
GN Name=REV;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CC NCBI_TaxID=11676;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=NL4-3;
CC MEDLINE=96036482; PubMed=7483282;
CC Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
CC Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
CC "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
CC from primary virus cultures using the polymerase chain reaction.";
CC Virology 213:80-86 (1995).
CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=NL4-3;
CC MEDLINE=86281827; PubMed=3016298;
CC Adachi A., Gendelman H.E., Koenig S., Folke T., Willey R., Rabson A.,
CC Martin M.A.;
CC "Production of acquired immunodeficiency syndrome-associated
CC retrovirus in human and nonhuman cells transfected with an infectious
CC molecular clone.";
CC J. Virol. 59:284-291 (1986).
CC [3]
CC SEQUENCE FROM N.A.
CC STRAIN=NL4-3;
CC Salminen M.S.;
CC Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC EMBL: U26942; AAB60576.1; -
CC DR GO; GO:0042025; C:host cell nucleus; IEA.
CC DR GO; GO:0003700; F:transcription factor activity; IEA.
CC DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
CC DR InterPro: IPR007110; IG-1like.
CC DR InterPro: IPR00625; REV_protein.
CC DR Pfam: PF00424; REV; 1.
CC SEQUENCE 116 AA; 13105 MW; 0FCF444DC9A7F3A9 CRC64;

Query Match 98.8%; Score 338; DB 2; Length 116;
Best Local Similarity 98.5%; Pred. No. 6.7e-33;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
Db 50 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 109
Qy 61 LESGTKE 67
Db 110 LESGTKE 116

RESULT 4
REV_HV1B2
ID REV_HV1B2 STANDARD; PRT; 116 AA.
AC P04618;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN Name=REV;
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CC NCBI_TaxID=11706;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=87299196; PubMed=3040055;
CC Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

```


RA Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS
 virus.";
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 CC -1- FUNCTION: Rev appears to act post-transcriptionally to relieve
 CC negative repression of Gag and Env production.
 CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
 CC -1- PFM: Phosphoprotein whose state of phosphorylation is mediated by
 CC a specific serine kinase activity present in the nucleus.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; K03455; AAB50257.1; -.
 DR PIR; J04968; J04968.
 DR HIV; K03455; REVSHXB2.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00424; REV, 1.
 KM AIDS; Nuclear protein; Phosphorylation; Transcription regulation.
 SQ SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 1; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPAY 60
 Db 50 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPTV 109

Qy 61 LESGTE 67
 Db 110 LESGTE 116

RESULT 5
 Q77Y21 PRELIMINARY; PRT; 116 AA.
 AC Q77Y21;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Rev.
 GN Name:rev;
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=57667;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4;
 RA MEDLINE=92309177; PubMed=1613662;
 RA Li J., Lord C.I., Haseltine W., Letvin N.L., Sodroski J.;
 RT "Infection of cynomolgus monkeys with a chimeric HIV-1/sivmac virus
 RT that expresses the HIV-1 envelope glycoproteins.";
 RL J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4;
 RA Reimann K.A., Li J.T., Voss G., Iekutis C., Tenner-Racz K., Racz P.,
 RA Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Colman R.G.,
 RA Sodroski J., Letvin N.L.;
 RL Submitted (Dec-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99098984; PubMed=9882298;
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
 RA Steenbeke T., Halloran M., Fanton J.W., Athelme M.K., Letvin N.L.,
 RA Sodroski J.G.;

RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
 RT responsible for the pathogenicity of a multiply passed simian-human
 RT immunodeficiency virus (SHIV-HXBc2).";
 RL J. Virol. 73:976-984(1999).
 DR EMBL; AF038399; AAB99974.1; -.
 DR EMBL; AF041850; AAD12140.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00424; REV, 1.
 SQ SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPAY 60
 Db 50 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPTV 109

Qy 61 LESGTE 67
 Db 110 LESGTE 116

RESULT 6
 Q77YF8 PRELIMINARY; PRT; 116 AA.
 AC Q77YF8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Rev.
 GN Name:rev;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA Petropoulos C.J.;
 RT "Appendix 2: Retroviral taxonomy, protein structure, sequences, and
 RT genetic maps.";
 RL (In) Coffin J.M. (eds.);
 RL RETROVIRUSES, pp.757-0; Cold Spring Harbor Laboratory Press, Cold
 RL Spring Harbor, New York, NY, USA (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chappey C.;
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF033819; AAC82592.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR000625; REV_protein.
 DR Pfam; PF00424; REV, 1.
 FT CHAIN 26 116 transmembrane envelope.
 SQ SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPAY 60
 Db 50 RQHSISERILSTYIGRSABVPVLPPLERLTLDNCNDCGTSCTGQVGSPOILVESPTV 109

Qy 61 LESGTE 67
 Db 110 LESGTE 116

RESULT 7
 AAB99974 PRELIMINARY; PRT; 116 AA.
 AC AAB99974;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Rev.
 GN REV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4, HXB2;
 RX MEDLINE=92309177; PubMed=1613662;
 RA Li J., Lord C.I., Haseltine W., Letvin N.L., Sodroski J.;
 RT "Infection of cynomolgus monkeys with a chimeric HIV-1/SIVmac virus
 that expresses the HIV-1 envelope glycoproteins."
 RL J. Acquir. Immune Defic. Syndr. 5:639-646(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SHIV-4, HXB2;
 RA Reimann K.A., Li J.T., Voss G., Lekutis C., Temner-Racz K., Racz P.,
 Lin W., Montefiori D.C., Lee-Parritz D.E., Lu Y., Colman R.G.,
 RA Sodroski J., Letvin N.L.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF038399; AAB99974.1; -
 SO SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
 DB 50 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116

RESULT 8
 AAD12140 PRELIMINARY; PRT; 116 AA.
 ID AAD12140
 AC AAD12140;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Rev protein.
 GN REV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99098984; PubMed=9882298;
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
 RA Steenbeke T., Halloran M., Fantom J.W., Axthelm M.K., Letvin N.L.,
 RA Sodroski J.G.;
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
 responsible for the pathogenicity of a multiply passaged simian-human
 immunodeficiency virus (SHIV-HXB2)."
 RL J. Virol. 73:976-984(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
 RA Halloran M., Axthelm M.W., Letvin N.L., Sodroski J.G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041850; AAD12140.1; -
 SO SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60

DB 50 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116

RESULT 9
 AAC82592 PRELIMINARY; PRT; 116 AA.
 ID AAC82592
 AC AAC82592;
 DT 02-MAR-2004 (TReMBLrel. 27, Created)
 DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
 DE Rev.
 GN REV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Petropoulos C.J.;
 RT "Appendix 2: Retroviral taxonomy, protein structure, sequences, and
 genetic maps."
 RL (In) Coffin J.M. (eds.);
 RL RETROVIRUSES, pp.757-0, Cold Spring Harbor Laboratory Press,
 RL Cold Spring Harbor, New York, NY, USA (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chappey C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF033819; AAC82592.1; -
 SO SEQUENCE 116 AA; 13075 MW; 4BCF5059C9A7F3B2 CRC64;

Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 2e-32;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
 DB 50 ROHSISERILSTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116

RESULT 10
 REV_HVILW STANDARD; PRT; 118 AA.
 ID REV_HVILW
 AC 070624;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE REV protein (Anti-repression transactivator protein) (ART/TRS).
 GN Name=REV;
 OS Human immunodeficiency virus type 1 (HM1.2.3 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=82834;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95127297; PubMed=782669;
 RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 CC -1- FUNCTION: Rev appears to act post-transcriptionally to relieve
 CC negative repression of Gag and Env production.
 CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
 CC -1- PTM: Phosphoprotein whose state of phosphorylation is mediated by

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CC      a specific serine kinase activity present in the nucleus.
CC      -----
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CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; U12055; AAA76688.1; -.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR000625; REV_protein.
DR      Pfam; PF00424; REV; 1.
DR      AIDS; Nuclear protein; Phosphorylation; Transcription regulation.
SQ      SEQUENCE 118 AA; 13169 MW; 5A4DD685E5CC546 CRC64;

Query Match
Best Local Similarity 97.7%; Score 334; DB 1; Length 118;
Matches 65; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPAV 60
DB      52 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPTV 111
QY      61 LESGTE 67
DB      112 LESGTE 118

RESULT 11
QY      099358      PRELIMINARY;      PRT;      201 AA.
AC      099358;
DT      01-NOV-1996 (TREMBlrel. 01, Created)
DT      01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      P28-rev.
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90244359; PubMed=2186172;
RA      Benko D.M., Schwartz S., Pavlakis G.N., Felber B.K.;
RT      "A novel human immunodeficiency virus type 1 protein, tev, shares
RT      sequences with tat, env, and rev proteins.";
RL      J. Virol. 64:2505-2518(1990).
CC      -1- FUNCTION: Transcriptional regulator that acts by binding to the
CC      trans-activating responsive sequence (TAR) RNA element and
CC      activates transcription initiation and/or elongation from the LTR
CC      promoter (By similarity).
CC      -----
DR      HSSP; P04610; 1TFW.
DR      EMBL; M37898; AAA44996.1; -.
DR      HSSP; P04610; 1TFW.
DR      GO; GO:0042025; C:host cell nucleus; IEA.
DR      GO; GO:0019031; C:viral envelope; IEA.
DR      GO; GO:0003700; F:transcription factor activity; IEA.
DR      GO; GO:0006335; P:regulation of transcription, DNA-dependent; IEA.
DR      InterPro; IPR000777; GP120.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR001831; IV Tat.
DR      InterPro; IPR000625; REV_protein.
DR      Pfam; PF00516; GP120; 1.
DR      Pfam; PF00424; REV; 1.
DR      Pfam; PF00539; Tat; 1.
DR      AIDS; Activator; Coat protein; Glycoprotein; Nuclear protein;
DR      RNA-binding; Transcription regulation; Transmembrane.
SQ      SEQUENCE 201 AA; 22842 MW; 1BDD60A70F191474 CRC64;

Query Match
Best Local Similarity 97.7%; Score 334; DB 2; Length 201;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPAV 60
DB      135 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPTV 194
QY      61 LESGTE 67
DB      195 LESGTE 201

RESULT 12
REV_HV1B1
ID      REV_HV1B1      STANDARD;      PRT;      116 AA.
AC      P04616;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      REV protein (Anti-repression transactivator protein) (ART/TRS).
GN      Name=REV;
OS      Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
OC      Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=85111123; PubMed=2578615;
RA      Ratner L., Haseltine W., Patarca R., Lyvak K.J., Starcich B.R.,
RA      Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA      Baumeister K., Ivanoff L., Patarca S.R., Dr., Pearson M.L.,
RA      Lautenberger J.A., Papas T.S., Grayeb J., Chang N.T., Gallo R.C.,
RA      Wong-Staal F.;
RT      "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL      Nature 313:277-284(1985).
CC      -1- FUNCTION: Rev appears to act post-transcriptionally to relieve
CC      negative repression of Gag and Env production.
CC      -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC      -1- PTM: Phosphoprotein whose state of phosphorylation is mediated by
CC      a specific serine kinase activity present in the nucleus.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL; M15654; AAA44200.1; -.
DR      HIV; M15654; REV_SBH102.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR000625; REV_protein.
DR      Pfam; PF00424; REV; 1.
DR      AIDS; Nuclear protein; Phosphorylation; Transcription regulation.
SQ      SEQUENCE 116 AA; 13037 MW; 30DA2E7AF302FBCD CRC64;

Query Match
Best Local Similarity 97.4%; Score 333; DB 1; Length 116;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPAV 60
DB      50 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTQGVSGQIIVESPTV 109
QY      61 LESGTE 67
DB      110 LESGTE 116

RESULT 13
QY      08Q2T0      PRELIMINARY;      PRT;      98 AA.
AC      08Q2T0;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)

```

```

DE Mutant rev protein d46.
GN Name=rev;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22157080; PubMed=12167277;
RA Fang J., Kubota S., Pomerantz R.J.;
RA "A trans-dominant negative HIV type 1 Rev with intact domains of
RT NLS/NOS and NES.";
RL AIDS Res. Hum. Retroviruses 18:705-709 (2002).
DR EMBL, AF493673; AAM18556.1; -.
DR GO, GO:0042025; C:host cell nucleus; IEA.
DR GO, GO:0003700; F:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR007110; IG-like.
DR Pfam, PF00424; REV_1.
SQ SEQUENCE 98 AA; 10833 MW; B5C56B6057A8B047 CRC64;

Query Match 97.1%; Score 332; DB 2; Length 98;
Best Local Similarity 95.5%; Pred. No. 2.9e-32;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPAV 60
DB 32 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPTI 91
QY 61 LESGKE 67
DB 92 LESGAKE 98

RESULT 14
08Q2T1 PRELIMINARY; PRT; 107 AA.
ID 08Q2T1
AC 08Q2T1;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mutant rev protein d23.
GN Name=rev;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22157080; PubMed=12167277;
RA Fang J., Kubota S., Pomerantz R.J.;
RA "A trans-dominant negative HIV type 1 Rev with intact domains of
RT NLS/NOS and NES.";
RL AIDS Res. Hum. Retroviruses 18:705-709 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Satoht K., Fang J., Pomerantz R.J.;
RA Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL, AF493672; AAM18555.1; -.
DR GO, GO:0042025; C:host cell nucleus; IEA.
DR GO, GO:0003700; F:transcription factor activity; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR007110; IG-like.
DR InterPro, IPR00625; REV_protein.
DR Pfam, PF00424; REV_1.
SQ SEQUENCE 107 AA; 12052 MW; 5536A0F1B6B1259 CRC64;

Query Match 97.1%; Score 332; DB 2; Length 107;
Best Local Similarity 95.5%; Pred. No. 3.2e-32;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPAV 60
DB 41 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPTI 100

```

```

QY 61 LESGKE 67
DB 101 LESGAKE 107

RESULT 15
REV_HV112 STANDARD; PRT; 116 AA.
ID REV_HV112
AC P04325;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN Name=REV;
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86177573; PubMed=3008154;
RA Arya S.K., Gallo R.C.;
RA "Three novel genes of human T-lymphotropic virus type III: immune
RT reactivity of their products with sera from acquired immune deficiency
RT syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=86230863; PubMed=3012355;
RA Sodirock J., Goh W.C., Rosen C., Dayton A., Terwilliger E.,
RA Haeltline W.;
RT Nature 321:412-417 (1986).
RT III replication."
CC -I- FUNCTION: Rev appears to act post-transcriptionally to relieve
CC negative repression of gag and env production.
CC -I- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -I- PTM: Phosphoprotein whose state of phosphorylation is mediated by
CC a specific serine kinase activity present in the nucleus.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk.)
CC -----
CC EMBL, M11840; AAA5000.1; -.
DR HIV, M11840; REVSPCV12.
DR InterPro, IPR007110; IG-like.
DR InterPro, IPR00625; REV_protein.
DR Pfam, PF00424; REV_1.
KW AIDS; Nuclear protein; Phosphorylation; Transcription regulation.
SQ SEQUENCE 116 AA; 13065 MW; EFAB7BEA247EPPF CRC64;

Query Match 97.1%; Score 332; DB 1; Length 116;
Best Local Similarity 95.5%; Pred. No. 3.6e-33;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPAV 60
DB 50 ROHSISERITSTYGRSAEPVPLQLPPLRLTLDCNEDCGTSGTGVGSPQILVESPTI 109
QY 61 LESGKE 67
DB 110 LESGAKE 116

```

Search completed: December 14, 2004, 16:48:14
 Job time : 214.725 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:04 ; Search time 190.113 Seconds
(without alignments)
126.424 Million cell updates/sec

Title: US-09-055-744A-9

Sequence: 1 RQHSISERLSTYLGRSAE.....VGSPQILVESPAVLESGTKE 67

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: A_Geneseq_23Sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	98.8	116	2	AAR78743
2	338	98.8	116	3	AAI10051
3	334	97.7	116	2	AAK48967
4	334	97.7	116	2	AAK57347
5	334	97.7	116	8	ADN36421
6	334	97.7	420	2	AAK53784
7	333	97.4	100	1	AAK70051
8	333	97.4	116	4	AAK85997
9	332	97.1	114	2	AAK08430
10	332	97.1	116	2	AAK08429
11	332	97.1	116	2	AAK38620
12	331	96.8	116	2	AAK48965
13	328	95.9	116	5	AAU11876
14	327.5	95.8	66	2	AAV45251
15	325	95.0	116	2	AAK77543
16	319	93.3	116	2	AAK08432
17	319	93.3	116	8	ADP20080
18	315	92.1	90	3	AAK69229
19	314	91.8	116	6	AAK55493
20	309	90.4	419	6	AAK34790
21	309	90.4	419	6	AAK34788
22	309	90.4	419	6	AAK34789
23	309	90.4	419	6	AAK34791
24	309	90.4	419	6	AAK34787
25	309	90.4	641	6	AAK34800

ALIGNMENTS

26	309	90.4	641	6	AAK34801	Human imm
27	309	90.4	842	6	AAK34802	Human imm
28	309	90.4	1006	6	AAK34808	Human imm
29	309	90.4	1006	6	AAK34809	Human imm
30	309	90.4	1006	6	AAK34810	Human imm
31	309	90.4	1006	6	AAK34807	Human imm
32	309	90.4	1064	6	AAK34803	Human imm
33	309	90.4	1064	6	AAK34806	Human imm
34	309	90.4	1064	6	AAK34805	Human imm
35	309	90.4	1064	6	AAK34804	Human imm
36	307	89.8	114	2	AAK08431	Human imm
37	301	88.0	116	2	ADK052529	Human imm
38	298	87.1	90	3	AAK69246	Human imm
39	297	86.8	116	2	AAK12260	Human imm
40	291.5	85.2	113	5	AAU11871	Human imm
41	289	84.5	116	8	ADK052540	Human imm
42	286	83.6	119	2	AAK09304	Human imm
43	283	82.7	3183	8	ADP84803	Human imm
44	278	81.3	117	3	AAK69329	Human imm
45	261	76.3	386	6	AAK34794	Human imm

RESULT 1
AAR78743 standard; protein: 116 AA.
AAR78743;
09-FEB-1996 (first entry)
Wild type REV HIV protein (residues 1 to 116).
TAT; REV; HIV; human immunodeficiency virus; trans-dominant variant; treat; prevent; viral infection; viral propagation; inhibit.
Human immunodeficiency virus.
FR2713651-A1.
16-JUN-1995.
13-DEC-1993; 93FR-00014914.
13-DEC-1993; 93FR-00014914.
(TRGE) TRANSGENE SA.
Mehra M, Sorg T;
WPI; 1995-217532/29.
Compn. conty. two trans-dominant variants of viral proteins - esp. of TAT and REV HIV proteins, useful for preventing or treating viral infection.
Disclosure; Page 19-20; 31pp; French.
The protein is that of residues 1 to 116 of the HIV (human immunodeficiency virus) REV protein. An antiviral compsn. comprising a first trans-dominant variant (esp. derived from HIV TAT; see AAR78742 and AAR7542) of a viral protein and a second trans-dominant variant of a different viral protein of the same virus (esp. derived from HIV REV; see AAR7543) are used to treat or prevent viral infection, esp. HIV. The trans-dominant variant viral proteins inhibit both infection of cells and viral propagation
Sequence 116 AA:
Query Match 98.8%; Score 338; DB 2; Length 116;
Best Local Similarity 98.5%; Pred. No. 1.3e-34;

```

Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPAV 60
Db 50 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPTV 109
QY 61 LESGKTE 67
Db 110 LESGKTE 116

RESULT 2
AAB10051
ID AAB10051 standard; protein, 116 AA.
AC AAB10051;
XX
XX
DT 12-SEP-2003 (revised)
DT 02-NOV-2000 (first entry)
XX
XX
DE HIV-1 rev protein.
XX
XX
KM Glycoprotein; gag; pol; GP-1; GP-2; anti-HIV; cytostatic; gene therapy;
KM treatment; infectious disease; HIV; AIDS; neoplasm; carcinoma; melanoma;
KM rev protein.
XX
XX
OS Human immunodeficiency virus 1.
XX
XX
PN EPI006196-A2.
XX
XX
PD 07-JUN-2000.
XX
XX
PF 25-NOV-1999; 99EP-00250415.
XX
XX
PR 26-NOV-1998; 98DE-01056463.
XX
XX
PA (PETT-) BETTE INST HEINRICH.
XX
XX
PI Von Laer MD;
XX
XX
DR WPI; 2000-378268/33.
XX
XX
N-PSDB; AAA40298; AAB10053; AAB10054.
XX
XX
PT New retroviral packing cell useful as pharmaceutical carrier in gene
PT therapy for treatment of HIV and neoplasms, comprises retroviral genes
PT and glycoproteins.
XX
XX
PS Disclosure; Page 45; 69pp; German.
XX
XX
CC This invention describes a novel retroviral packing cell (I), comprising
CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV
CC coding gene gp, or a part of these. The products of the invention have
CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is
CC useful for in vitro infection of cells, especially hematopoietic stem
CC cells, for expression of transgenes in cells and as a pharmaceutical
CC carrier for gene therapy. (I) is therefore useful in the treatment of
CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and
CC other diseases. This sequence represents the Human immunodeficiency virus
CC (HIV-1) rev protein described in the method of the invention. (Updated on
CC 12-SEP-2003 to standardise OS field)
XX
XX
SQ Sequence 116 AA;
Query Match 98.8%; Score 338; DB 3; Length 116;
Best Local Similarity 98.5%; Pred. No. 1.3e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPAV 60
Db 50 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPTV 109
QY 61 LESGKTE 67
Db 110 LESGKTE 67

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Db 110 LESGKTE 116

RESULT 3
AAR48967
ID AAR48967 standard; protein, 116 AA.
AC AAR48967;
XX
XX
XX
DT 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX
XX
DE Diversified HIV-1 REV.
XX
XX
KM HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
KM naturally occurring virus; NOV; translation; replication; infectivity;
KM hepatitis B; HIV-2; SIV; flip-over PCR.
XX
XX
OS Synthetic.
XX
XX
PN MO9403596-A1.
XX
XX
PD 17-FEB-1994.
XX
XX
PF 30-JUL-1993; 93WO-US007179.
XX
XX
PR 30-JUL-1992; 92US-00921104.
XX
XX
PA (UYHA-) UNIV HAWAII.
XX
XX
PI Hu W, Wang J;
XX
XX
DR WPI; 1994-065685/08.
XX
XX
N-PSDB; AAQ57918.
XX
XX
PT New antisense viruses and anti-sense-ribozyme viruses - used for treating
PT or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.
XX
XX
PS Disclosure; Page 142; 167pp; English.
XX
XX
CC This sequence is a diversified HIV-1 REV protein. The DNA encoding this
CC sequence was produced using the primer sequences given in AAQ57919-26.
CC This sequence was used in the production of an antisense virus. Antisense
CC or truncated RNAs expressed by viruses such as this bind to the mRNAs
CC expressed by the naturally occurring viruses (NOVs) and prevent the mRNAs
CC from being translated into proteins, thereby preventing the NOV from
CC replicating. The antisense viruses maintain the infectivity of the NOVs,
CC allowing antisense RNAs to reach the mRNAs of the natural viruses.
CC Antisense viruses such as these may be used for treating or preventing a
CC viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis
CC B infection. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
SQ Sequence 116 AA;
Query Match 97.7%; Score 334; DB 2; Length 116;
Best Local Similarity 97.0%; Pred. No. 4.1e-34;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPAV 60
Db 50 ROHSISERILSTYIGRSABEVPVLQPLPRLTLTDNCNDCGSGTGQVGSPOILVESPTV 109
QY 61 LESGKTE 67
Db 110 LESGKTE 116

RESULT 4
AAR57347
ID AAR57347 standard; peptide, 116 AA.
AC AAR57347;
XX
XX
XX

```

DT 25-MAR-2003 (revised)
 DT 07-MAR-1995 (first entry)
 XX
 DE Peptide fragment of HIV 3HXB2 rev protein.
 XX
 KM Human immunodeficiency virus; HIV; tat; rev; transactivator protein;
 KM regulatory viron protein; treatment; therapy.
 XX
 OS Human immunodeficiency virus.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 FT 35..50
 FT /note= "Region responsible for RNA binding and
 FT nuclear/nucleolar localisation."
 FT 73..83
 FT /note= "Leucine motif."
 FT Region
 FT WO9415634-A1.
 XX
 PN 21-JUL-1994.
 XX
 PD 21-JUL-1994.
 XX
 PF 30-DEC-1993; 93WO-US012680.
 XX
 PR 30-DEC-1992; 92US-00997734.
 XX
 PA (RATH/) RATH M.
 PI RATH M;
 PT WPI; 1994-248897/30.
 DR
 XX
 PT Signal sequence fragments of Rev and Tat regulatory proteins - for
 PT treatment and prevention of human immunodeficiency virus infection.
 XX
 PS Disclosure; Fig 2; 13pp; English.
 XX
 CC The regulator of viron expression (rev) is a regulatory protein involved
 CC in HIV gene expression and pathogenicity. The virus life cycle is divided
 CC into an early phase during which the rev protein is made and a late phase
 CC in which virus structural proteins are made and virus particles are
 CC assembled. The rev protein mediates the switch from the early to the late
 CC phase. A strong basic amino acid region of the rev protein determines its
 CC binding to RNA and also specifies nuclear and nucleolar localisation.
 CC This peptide region of the rev protein is responsible for the specific
 CC binding of rev to the rev responsive element. The protein can be
 CC inhibited in two ways (1) by the competitive inhibition of its binding to
 CC viral RNA via synthetic analogues of the signal sequences; and (2) by
 CC antibodies raised against these signal sequences which block the binding
 CC of the protein to viral RNA. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 CC
 XX
 SQ Sequence 116 AA;
 Query Match 97.7%; Score 334; DB 2; Length 116;
 Best Local Similarity 97.0%; Pred. No. 4.1e-34;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTGTGCGSPQIIVESPAV 60
 DB 50 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTGTGCGSPQIIVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116
 DT 15-JUL-2004 (first entry)

XX
 DE HIV protein for anti-HIV vaccine.
 XX
 KM anti-HIV; vaccine; HIV; promoter; viral particle; immunization.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO2004035006-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 17-OCT-2003; 2003WO-US033112.
 XX
 PR 18-OCT-2002; 2002US-0419465P.
 XX
 PA (AARON-) AARON DIAMOND AIDS RES CENT.
 PI Huang Y, Ho DD, Chen Z;
 PT WPI; 2004-348328/32.
 DR N-PSDB; ADN36420.
 DR
 XX
 PF Nucleic acid vector comprising at least one HIV sequence operably linked
 PT to a promoter and encoding a protein that does not assemble into viral
 PT particles, useful in immunizing a subject against HIV infection.
 XX
 PS Disclosure; SEQ ID NO 35; 166pp; English.
 XX
 CC The invention relates to a nucleic acid vector comprising at least one
 CC HIV sequence operably linked to a promoter and encoding a protein that
 CC does not assemble into viral particles. The nucleic acid vector is useful
 CC in immunizing a subject against HIV infection. This sequence corresponds
 CC to a nucleic acid used in the invention.
 CC
 XX
 SQ Sequence 116 AA;
 Query Match 97.7%; Score 334; DB 8; Length 116;
 Best Local Similarity 97.0%; Pred. No. 4.1e-34;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTGTGCGSPQIIVESPAV 60
 DB 50 RQHSISERITSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTGTGCGSPQIIVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 28-DEC-1994 (first entry)
 DE Translation of mutated HIV-1 in the region of the gp41 polypeptide.
 XX
 KM Human immunodeficiency virus; HIV-1; AIDS; lentivirus; TM protein;
 KM extracellular protein; transmembrane protein; gp41.
 XX
 OS Human immunodeficiency virus 1.
 XX
 FH Key
 FT Misc-difference 1..420
 FT /note= "X in AA sequence corresp. to a stop codon in the
 FT nucleic acid sequence AA066275."
 FT
 PN WO9412533-A1.

PD 09-JUN-1994.
 XX
 PF 12-JAN-1993; 93WO-US000212.
 XX
 PR 23-NOV-1992; 92US-00979975.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Essek ME, Yu X, Lee TH;
 XX
 DR WPI: 1994-200197/24.
 DR N-PSDB; AA066275.
 XX
 PT Method for treating HIV patients - comprises administration of mutated
 PT Gp41 polypeptide.
 XX
 PS Example; Fig 1; 54pp; English.
 XX
 CC The wild type provirus clone of HIV-1 is HXB2R3. In frame stop codons
 CC were generated at different positions in the gp41 coding region (see
 CC AA066275). AA066275 corresp. to bps 7631-8890 of wt HIV-1. The AAs of the
 CC overlapping rev ORF were not affected by the nucleotide substitutions.
 CC Figure 1 shows AA066275 translated in 3 reading frames. AAR53784 is the
 CC AA sequence of one of these translations (updated on 25-MAR-2003 to
 CC correct FN field.) (Updated on 16-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 420 AA;
 Query Match 97.7%; Score 334; DB 2; Length 420;
 Best Local Similarity 97.0%; Pred. No. 2.1e-33;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSQQLIVESPV 60
 DB 274 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSQQLIVESPTV 333
 QY 61 LESGTKE 67
 DB 334 LESGTKE 340
 RESULT 7
 AAF70051
 ID AAF70051 standard; protein; 100 AA.
 XX
 AC AAF70051;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-OCT-2002 (revised)
 DT 27-JAN-1991 (first entry)
 XX
 DE Coding exon 1 of HIV virus art gene.
 XX
 KM HIV virus; art gene product; AIDS.
 XX
 OS Human immunodeficiency virus.
 XX
 PN EP246882-A.
 XX
 PD 25-NOV-1987.
 XX
 PF 20-MAY-1987; 87EP-00304493.
 XX
 PR 20-MAY-1986; 86US-00865151.
 XX
 PA (DAND) DANA-FARBER CANCER.
 XX
 PI Haseltine WA, Rosen GA, Soddroski JG, Goh WC;
 XX
 DR WPI: 1987-329080/47.
 DR N-PSDB; AAN70050.
 XX
 PT HTLV-III art gene sequence - used for screening for cpds. that inhibit

PT HTLV-III replication, producing antibodies and diagnosis or therapy of
 PT AIDS.
 XX
 PS Disclosure; Fig 1; 22pp; English.
 XX
 CC The protein sequence encodes coding exon II of the HIV virus art gene.
 CC The art gene and gene product may be used in AIDS therapy and diagnosis.
 CC (See also AAN70049) (Updated on 03-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 100 AA;
 Query Match 97.4%; Score 333; DB 1; Length 100;
 Best Local Similarity 97.0%; Pred. No. 4.6e-34;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSQQLIVESPV 60
 DB 34 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSQQLIVESPTV 93
 QY 61 LESGTKE 67
 DB 94 LESGTKE 100
 RESULT 8
 AAB85997
 ID AAB85997 standard; protein; 116 AA.
 XX
 AC AAB85997;
 XX
 DT 11-SEP-2003 (revised)
 DT 30-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of HIV-1 isolate BH10 rev protein.
 XX
 KM HIV-1; gp120; BH10; vaccine; immunization; rev protein.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US6268484-B1.
 XX
 PD 31-JUL-2001.
 XX
 PF 30-JUL-1998; 98US-00124900.
 XX
 PR 19-APR-1995; 95WO-EP001481.
 PR 07-JUN-1995; 95US-00478536.
 XX
 PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.
 XX
 PI Katinger H, Buchacher A, Ernst W, Ballaun C, Purscher M;
 PI Trkola A, Predl R, Schmatz C, Klima A, Steindl F, Muster T;
 XX
 DR WPI: 2001-556601/62.
 DR N-PSDB; AAN76385.
 XX
 PT New anti-idiotypic antibodies consisting of one or both amino acid
 PT sequences corresponding to amino acid positions 79-84 or 326-400 of the
 PT processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1
 PT infections.
 XX
 PS Claim 1; Col 31-32; 27pp; English.
 XX
 CC The invention relates to a peptide fragment comprising of amino acid
 CC sequences corresponding to sequences within the processed gp120 of HIV-1
 CC isolate BH10 (GenBank accession M15654). The peptides are useful in the
 CC detection, prevention and treatment of HIV-1 infections, and in AIDS
 CC therapy. The antibodies are especially useful as vaccines for active and
 CC passive immunization, or for the detection and/or determination of HIV-1
 CC infected cells and/or HIV-1 viruses. The present sequence represents the
 CC amino acid sequence of a rev protein from HIV-1 isolate BH10 (GenBank

CC accession M15654. (Updated on 11-SEP-2003 to standardise OS field)
 XX Sequence 116 AA;

Query Match 97.4%; Score 333; DB 4; Length 116;
 Best Local Similarity 97.0%; Pred. No. 5.5e-34;
 Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQHSISERLSTYLGSAAPVPLQLPPLRLTDCNEDCGTSGTGVGSPQIIIVESPAV 60
 DB 50 RQHSISERLSTYLGSAAPVPLQLPPLRLTDCNEDCGTSGTGVGSPQIIIVESPTV 109

QY 61 LESGTE 67
 DB 110 LESGAKE 116

RESULT 9

AA08430
 ID AAR08430 standard; protein; 114 AA.

AC AAR08430;

DT 25-MAR-2003 (revised)
 DT 07-MAR-1991 (first entry)

XX HIV-1 Rev M6 mutant transdominant repressor of viral replication.

XX HIV 1; rev gene; transdominant repressor; anti-viral agent; AIDS.

XX Human immunodeficiency virus 1.

XX WO9014427-A.

XX 29-NOV-1990.

XX 25-MAY-1989; 89US-00356878.

XX 25-MAY-1989; 89US-00356878.

XX 07-JUL-1989; 89GB-00015602.

XX 30-OCT-1989; 89GB-00024396.

XX 29-NOV-1989; 89US-00442670.

XX (SANO) SANDOZ LTD.

XX (UYDU-) UNIV DUKE.

XX Bachmayer H, Boehnlein E, Cullen BR, Greene WC, Hauber J;

XX WPI; 1990-375994/50.

XX N-PSDB; AAQ07017.

XX Viral gene expression multivalent repressors - from rev gene prod. of HIV

XX -1 or rex prod. of HTLV-1 for intracellular immunisation.

XX Disclosure; Fig 7; 10pp; English.

XX Mutants of the rev gene product act as transdominant repressors of wild-

XX type rev and/or rex gene activity. In mutant M6 amino acids 41 to 44 (Arg

XX -Arg-Arg-Arg) of the wild-type rev product are replaced by amino acids 41

XX (Asp) and 42 (Leu) of the mutant. Asm(40) of wild-type rev is replaced by

XX Lys. Analysis of the ability of M6 to inhibit viral replication showed it

XX to be effective in inhibiting HIV-1 rex gene function and HIV-1 rev gene

XX function. For example, M6 produced dose-related inhibition of HIV-1 p24

XX gag protein production. See also AAQ07008-007016 and AAQ07018-007019.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 114 AA;

DB 48 RQHSISERLSTYLGSAAPVPLQLPPLRLTDCNEDCGTSGTGVGSPQIIIVESPTI 107
 QY 61 LESGTE 67
 DB 108 LESGAKE 114

RESULT 10

AA08429
 ID AAR08429 standard; protein; 116 AA.

AC AAR08429;

DT 25-MAR-2003 (revised)
 DT 07-MAR-1991 (first entry)

XX HIV-1 Rev M1 mutant transdominant repressor of viral replication.

XX HIV 1; rev gene; transdominant repressor; anti-viral agent; AIDS.

XX Human immunodeficiency virus 1.

XX WO9014427-A.

XX 29-NOV-1990.

XX 25-MAY-1989; 89US-00356878.

XX 25-MAY-1989; 89US-00356878.

XX 07-JUL-1989; 89GB-00015602.

XX 30-OCT-1989; 89GB-00024396.

XX 29-NOV-1989; 89US-00442670.

XX (SANO) SANDOZ LTD.

XX (UYDU-) UNIV DUKE.

XX Bachmayer H, Boehnlein E, Cullen BR, Greene WC, Hauber J;

XX WPI; 1990-375994/50.

XX N-PSDB; AAQ07016.

XX Viral gene expression multivalent repressors - from rev gene prod. of HIV

XX -1 or rex prod. of HTLV-1 for intracellular immunisation.

XX Disclosure; Fig 7; 10pp; English.

XX Mutants of the rev gene product act as transdominant repressors of wild-

XX type rev and/or rex gene activity. In this mutant amino acids Arg(4) and

XX Ser(5) have been substituted by Asp and Leu, respectively. Analysis of

XX the ability of M1 to inhibit replication of HIV-1 showed it to be a

XX recessive negative mutant. It did not produce dose-related inhibition of

XX HIV-1 p24 gag protein production. See also AAQ07008-007015 and AAQ07017-

XX 007019. (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 116 AA;

Query Match 97.1%; Score 332; DB 2; Length 116;
 Best Local Similarity 95.5%; Pred. No. 7.4e-34;
 Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQHSISERLSTYLGSAAPVPLQLPPLRLTDCNEDCGTSGTGVGSPQIIIVESPAV 60
 DB 50 RQHSISERLSTYLGSAAPVPLQLPPLRLTDCNEDCGTSGTGVGSPQIIIVESPTI 109

QY 61 LESGTE 67
 DB 110 LESGAKE 116

RESULT 11

AA08620
 ID AAR08620 standard; protein; 116 AA.

```

XX AAR38620;
AC 25-MAR-2003 (revised)
DT 13-DEC-1993 (first entry)
XX
DE Sequence of the HIV-1 REV protein.
XX
XX Human immunodeficiency virus 1; HIV-1; regulatory factor;
XX viral replication; RNA binding.
XX
OS Human immunodeficiency virus 1.
XX
XX Key Location/Qualifiers
XX Domain 38..51
XX /label= Arginine-rich
XX
XX MO312234-A1.
XX
XX 24-JUN-1993.
XX
XX 11-DEC-1992; 92WO-US010770.
XX
XX 13-DEC-1991; 91US-00808452.
XX 21-JAN-1992; 92US-00826934.
XX
XX (STRI ) SRI INT.
XX
XX Jayasena SD, Johnston BH;
XX
XX WPI; 1993-214176/26.
XX
XX Viral polypeptide(s) with site-specific RNA binding - contain moiety to
XX cleave RNA backbone and are used to inhibit HIV antigen expression in
XX infected cells.
XX
XX
XX Claim 2; Fig 4; 94pp; English.
XX
XX HIV-1 REV is an RNA-binding protein. It is a regulatory factor essential
XX for viral replication and it is required for the prodn. of viral
XX structural proteins. It appears to exert its effect at the level of
XX splicing and perhaps transport of viral mRNA into the cytoplasm; further
XX REV appears to increase the stability of unspliced HIV mRNA. The REV
XX protein is encoded by two exons. An Arg-rich domain acts as the nuclear
XX targeting domain. Mutational analysis has demonstrated that some C-
XX terminal deletion mutants of the REV protein are non-functional but are
XX trans-dominant. The action of REV requires the presence of a target
XX sequence termed REV response element (AA044156) located in the HIV
XX envelope gene. RRE has been mapped to a 234-bp region capable of forming
XX four stem-loop structures and one branched stem-loop structure. Foot-
XX printing data suggest that REV binds to six nts in one stem structure and
XX to three nts in an adjacent stem-loop structure of the RRE. A 40 nt
XX region in stem-loop II (AA044157) has been implicated as the minimum REV
XX binding region. Both wt RRE (AA044156) and the truncated version
XX (AA044157) are synthesized by in vitro transcription using T7 RNA
XX polymerase. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 116 AA;
XX
XX Query Match 97.1%; Score 332; DB 2; Length 116;
XX Best Local Similarity 95.5%; Pred. No. 7.4e-34;
XX Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 ROHSISERILSTYLSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVGSPQIIVESPAV 60
DB 50 ROHSISERILSTYLSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVGSPQIIVESPTI 109
QY 61 LESGTXE 67
DB 110 LESGAKE 116

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AAR48965
ID AAR48965 standard; protein; 116 AA.
XX
XX AAR48965;
AC 25-MAR-2003 (revised)
DT 12-SEP-1994 (first entry)
XX
XX Full length REV.
XX
XX HIV-1; HXB2; antisense; sequence inversion; antisense virus; infection;
XX naturally occurring virus; NOV; translation; replication; infectivity;
XX hepatitis B; HIV-2; SIV; flip-over PCR.
XX
XX Synthetic.
XX
XX MO9403596-A1.
XX
XX 17-FEB-1994.
XX
XX 30-JUL-1993; 93WO-US007179.
XX
XX 30-JUL-1992; 92US-00921104.
XX
XX (UYHA-) UNIV HAWAII.
XX
XX Hu W, Wang J;
XX
XX WPI; 1994-065685/08.
XX
XX N-PSDB; AAQ57692.
XX
XX New antisense viruses and anti-sense-ribozyme viruses - used for treating
XX or preventing viral infections, partic. HIV-1, HIV-2 or SIV infection.
XX
XX Disclosure; Page 126; 167pp; English.
XX
XX This sequence is encoded by a fusion sequence in which the full length
XX tat and rev genes are linked, overlapping in different reading frames.
XX The DNA sequence was used in the production of an antisense virus.
XX Antisense or truncated RNAs expressed by viruses such as this bind to the
XX mRNAs expressed by the naturally occurring viruses (NOVs) and prevent the
XX mRNAs from being translated into proteins, thereby preventing the NOV
XX from replicating. The antisense viruses maintain the infectivity of the
XX NOVs, allowing antisense RNAs to reach the mRNAs of the natural viruses.
XX Antisense viruses such as these may be used for treating or preventing a
XX viral infection, particularly HIV-1, HIV-2 or SIV infection or hepatitis
XX B infection. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 116 AA;
XX
XX Query Match 96.8%; Score 331; DB 2; Length 116;
XX Best Local Similarity 95.5%; Pred. No. 9.9e-34;
XX Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 ROHSISERILSTYLSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVGSPQIIVESPAV 60
DB 50 ROHSISERILSTYLSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVGSPQIIVESPTV 109
QY 61 LESGTXE 67
DB 110 LESGTXE 116

```

XX T0 terminator; pGAL/J55; DNA vaccine; anti-HIV; virucide;
 KM Human Immunodeficiency Virus; HIV; Gag; HIV gp120; HIV Pol; HIV Env;
 KM HIV VLP; measles fusion protein; measles haemagglutinin;
 KM measles nucleoprotein; influenza haemagglutinin; C3d gene;
 KM cell-mediated immune response; humoral immune response; infection.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200192470-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 02-MAR-2001; 2001WO-US006795.
 XX
 PR 02-MAR-2000; 2000US-0186364P.
 XX
 PR 01-DEC-2000; 2000US-0251083P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Robinson HL, Smith JM, Rose TM, Bright RA, Hua J, Ellenberger D;
 XX
 DR WPI; 2002-075465/10.
 DR N-PSDB; AAS19260.
 XX
 PT Novel pGA vector useful for immunizing patient against measles, influenza
 PT has termination sequence encoding lambda T0 terminator and a eukaryotic
 PT transcription cassette with vaccine insert encoding immunogens of
 PT pathogens.
 XX
 PS Example 5; Fig 18; 174pp; English.
 XX
 CC The invention relates to a vector (a pGA construct) comprising a
 CC termination sequence coding for the lambda T0 terminator, a prokaryotic
 CC origin of replication, a selectable marker gene and a eukaryotic
 CC transcription cassette comprising a vaccine insert encoding one or more
 CC immunogens derived from a pathogen e.g. Human Immunodeficiency Virus
 CC (HIV) Gag, HIV gp120, HIV Pol, HIV Env, HIV VLP, or its mutants, measles
 CC fusion protein, measles haemagglutinin, measles nucleoprotein, influenza
 CC haemagglutinin, or its mutants, or subsequences, and optionally at least
 CC one C3d gene, is useful for immunising or treating a patient, when
 CC administered by an intramuscular or intradermal route. The immunisation
 CC method using pGA elicit both cell-mediated and humoral immune responses
 CC that may limit the infection, spread or growth of the pathogen and result
 CC in protection against subsequent challenge against the pathogen. The
 CC terminator sequence present prevents read-through from the Kanamycin
 CC cassette into vaccine sequences while the plasmid is being produced in
 CC bacteria. Prevention of transcriptional read-through stabilises vaccine
 CC insert sequences by limiting the exposure of secondary structures that
 CC can be recognised by bacterial endonucleases. The present sequence is the
 CC HIV rev protein from pGAL/J55 vector (the pGA2 vector expressing HIV gag,
 CC pol, tat, vpu, rev and env). (Updated on 29-AUG-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 116 AA;
 XX
 Query Match 95.9%; Score 328; DB 5; Length 116;
 Best Local Similarity 95.5%; Pred. No. 2.4e-33;
 Matches 64; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 RQHSISRILSTVYGRSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
 DB 50 RQHSISRILSTVYGRSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 109
 QY 61 LESGTKE 67
 DB 110 LESGAKE 116

AC AAY45251;
 XX
 DT 17-OCT-2003 (revised)
 DT 12-JAN-2000 (first entry)
 XX
 DE HIV-1 (LAI) Rev protein 52-116 lipopeptide CLP-164.
 XX
 KM HIV-1; Rev protein; HLA-A2-restricted CTL motif; T-cell epitope;
 KM cytotoxic T-cell response; immune system; T-helper cell; immunisation;
 KM vaccine; infection; AIDS; acquired immunodeficiency syndrome.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN MO9951267-A1.
 XX
 PD 14-OCT-1999.
 XX
 PF 01-APR-1999; 99WO-CA000287.
 XX
 PR 07-APR-1998; 98US-00055744.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Sia CDY, Chong P, Klein MH;
 XX
 DR WPI; 1999-620170/53.
 XX
 PT Generating an HIV-specific cytotoxic T-cell response, useful to immunize
 PT against HIV.
 XX
 PS Claim 12; Page 17; 35pp; English.
 XX
 CC The present invention describes a human immunodeficiency virus (HIV) -
 CC specific cytotoxic T-cell (CTL) response which is generated in a host by
 CC first administering a T-cell helper molecule to prime the immune system T
 CC -helper cells, and then administering a mixture of the helper and a T-
 CC cell inducing HIV-derived molecule. Also described are peptides having
 CC the sequence of amino acids 52-116 of the Rev protein of HIV-1 isolate
 CC LAI or a corresponding sequence from another HIV-1 isolate, capable of
 CC eliciting a CTL response. The method provides a novel protocol for
 CC achieving a HIV-specific CTL response in hosts, including humans, useful
 CC for immunisation against HIV, the causal agent of acquired
 CC immunodeficiency syndrome (AIDS). The peptides may be used in the
 CC preparation of vaccines for use in such immunisation protocols. No
 CC effective vaccination protocol or vaccines to protect humans from HIV
 CC infection currently exist. The Rev protein is also expressed early in the
 CC HIV life cycle, so that peptides based on Rev may induce CTL effector
 CC responses capable of killing virus-infected cells at an early stage,
 CC limiting virus spread. The present sequence represents an HIV-1 (LAI) Rev
 CC protein 52-116 lipopeptide, which is used in the exemplification of the
 CC present invention. (Updated on 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 66 AA;
 XX
 Query Match 95.8%; Score 327.5; DB 2; Length 66;
 Best Local Similarity 98.5%; Pred. No. 1.4e-33;
 Matches 66; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 RQHSISRILSTVYGRSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 60
 DB 1 RQHSISRILSTVYGRSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQILVESPAV 59
 QY 61 LESGTKE 67
 DB 60 LESGTKE 66

RESULT 14
 AAY45251
 ID AAY45251 standard; peptide; 66 AA.
 XX

RESULT 15
 AAR77543
 ID AAR77543 standard; protein; 116 AA.
 XX
 AC AAR77543;
 XX

DT 09-FEB-1996 (first entry)
 XX Trans-dominant variant of REV HIV protein (residues 1 to 116).
 DE
 XX TAT; REV; HIV; human immunodeficiency virus; trans-dominant variant;
 KM treat; prevent; viral infection; viral propagation; inhibit.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 74 /label= Q74G
 FT /note= "substitution from wild type"
 FT Misc-difference 75 /label= L75S
 FT /note= "substitution from wild type"
 XX
 XX FR2713651-A1.
 XX 16-JUN-1995.
 XX
 XX 13-DEC-1993; 93FR-00014914.
 XX PF
 XX 13-DEC-1993; 93FR-00014914.
 XX PR
 XX (TRGE) TRANSGENE SA.
 XX PA
 XX Mehtail M, Sorg T;
 XX PI
 XX WPI; 1995-217532/29.
 DR
 XX
 XX Compn. contg. two trans-dominant variants of viral proteins - esp. of
 PT TAT and REV HIV proteins, useful for preventing or treating viral
 PT infection.
 XX
 PS Claim 5; Page 19-20; 31pp; French.
 XX
 CC The protein is that of a trans-dominant variant derived from residues 1
 CC to 116 of the HIV (human immunodeficiency virus) REV protein. An
 CC antiviral compn. comprising a first trans-dominant variant (esp. derived
 CC from HIV TAT; see AAR76742 and AAR7542) of a viral protein and a second
 CC trans-dominant variant of a different viral protein of the same virus
 CC (esp. derived from HIV REV; see AAR76743) are used to treat or prevent
 CC viral infection, esp. HIV. The trans-dominant variant viral proteins
 CC inhibit both infection of cells and viral propagation
 XX
 SQ Sequence 116 AA;

Query Match 95.0%; Score 325; DB 2; Length 116;
 Best Local Similarity 95.5%; Pred. No. 5.7e-33;
 Matches 64; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RQHSISERISTYLGSAEVPPLQLPPLERLTLDQNECGTSGTQGVSPQILVESPAV 60
 DB 50 RQHSISERISTYLGSAEVPPLQLPPLERLTLDQNECGTSGTQGVSPQILVESPTV 109
 QY 61 LESGTKE 67
 DB 110 LESGTKE 116

Search completed: December 14, 2004, 16:42:00
 Job time : 192.113 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 45.225 Seconds
(without alignments)
98.249 Million cell updates/sec

Title: US-09-055-744A-9
Perfect score: 342
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Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	338	98.8	91	3	US-08-488-551B-638
2	338	98.8	106	3	US-08-388-353-638
3	338	98.8	116	2	US-08-505-210-2
4	338	98.8	116	3	US-09-099-333-2
5	338	98.8	116	4	US-09-309-572-21
6	338	98.8	116	4	US-09-718-096-21
7	333	97.1	116	3	US-09-124-900-7
8	332	97.1	116	3	US-07-808-452-6
9	332	97.1	116	5	PCT-US92-10770-6
10	300	87.7	94	3	US-08-488-551B-640
11	300	87.7	107	3	US-08-388-353-640
12	288	84.2	105	3	US-08-488-551B-639
13	288	84.2	108	3	US-08-388-353-639
14	148	43.3	103	4	US-09-319-588C-16
15	144	42.1	759	4	US-09-337-387-12
16	141	41.2	26	2	US-08-467-587A-5
17	138	40.4	26	2	US-08-467-587A-26
18	136	39.8	26	2	US-08-467-587A-20
19	136	39.8	26	2	US-08-467-587A-21
20	136	39.8	26	2	US-08-467-587A-22
21	134	39.2	26	2	US-08-467-587A-27
22	133	38.9	26	2	US-08-467-587A-6
23	133	38.9	26	2	US-08-467-587A-13
24	132	38.6	26	2	US-08-467-587A-8
25	132	38.6	26	2	US-08-467-587A-25
26	131	38.3	26	2	US-08-467-587A-14
27	128	37.4	23	5	PCT-US95-09589-7

28	128	37.4	23	5	PCT-US95-09589A-7	Sequence 7, Appli
29	128	37.4	26	2	US-08-467-587A-9	Sequence 9, Appli
30	127	37.1	26	2	US-08-467-587A-15	Sequence 15, Appli
31	126	36.8	26	2	US-08-467-587A-11	Sequence 11, Appli
32	126	36.8	26	2	US-08-467-587A-23	Sequence 23, Appli
33	126	36.8	26	2	US-08-467-587A-24	Sequence 24, Appli
34	125	36.5	26	2	US-08-467-587A-7	Sequence 7, Appli
35	124	36.3	26	2	US-08-467-587A-10	Sequence 10, Appli
36	123	36.0	23	2	US-08-687-702-8	Sequence 8, Appli
37	123	36.0	23	2	US-08-687-702-9	Sequence 9, Appli
38	123	36.0	26	2	US-08-467-587A-12	Sequence 12, Appli
39	123	36.0	26	2	US-08-467-587A-16	Sequence 16, Appli
40	122	35.7	26	2	US-08-467-587A-18	Sequence 18, Appli
41	121	35.4	23	2	US-08-687-702-10	Sequence 10, Appli
42	118	34.5	23	2	US-08-687-702-5	Sequence 5, Appli
43	116	33.9	26	2	US-08-467-587A-17	Sequence 17, Appli
44	115	33.6	26	2	US-08-467-587A-19	Sequence 19, Appli
45	112	32.7	23	2	US-08-687-702-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-488-551B-638
Sequence 638, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 638:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-551B-638

Query Match 98.8%; Score 338; DB 3; Length 91;
Best Local Similarity 98.5%; Pred. No. 2,6e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 25 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 84

QY 61 LESGTKE 67
DB 85 LESGTKE 91

RESULT 2

US-08-388-353-638
; Sequence 638, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digilio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 638:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-388-353-638

Query Match 98.8%; Score 338; DB 3; Length 106;
Best Local Similarity 98.5%; Pred. No. 3.1e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 25 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 84

QY 61 LESGTKE 67
DB 85 LESGTKE 91

RESULT 3

US-08-505-210-2
; Sequence 2, Application US/08505210
; Patent No. 5981258
; GENERAL INFORMATION:
; APPLICANT: MEHTALI, Majid
; APPLICANT: GUS, Tania
; TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS
; TITLE OF INVENTION: OF VIRAL PROTEINS FOR OBTAINING AN ANTIVIRAL EFFECT
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: 1737 King Street, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22314-2756
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,210
; FILING DATE: 14-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,248
; FILING DATE: 21-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/01457
; FILING DATE: 13-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dadio, Susan M.
; REGISTRATION NUMBER: 40,372
; REFERENCE/DOCKET NUMBER: 01753-066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-6621
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Human immunodeficiency virus type 1
; STRAIN: Lai
; INDIVIDUAL ISOLATE: sequence of the rev protein of the
; INDIVIDUAL ISOLATE: HIV-1 virus
; US-08-505-210-2

Query Match 98.8%; Score 338; DB 2; Length 116;
Best Local Similarity 98.5%; Pred. No. 3.5e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 50 ROHSISERISTYIGRSAPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 109

QY 61 LESGTKE 67
DB 110 LESGTKE 116

RESULT 4

US-09-099-333-2
; Sequence 2, Application US/09099333A
; Patent No. 6228369
; GENERAL INFORMATION:
; APPLICANT: MEHTALI, Majid

APPLICANT: Guss, Tania
TITLE OF INVENTION: COMPOSITION OF TRANS-DOMINANT VARIANTS OF VIRAL
FILE OF INVENTION: PROTEIN FOR OBTAINING AN ANTI-VIRAL EFFECT
FILE REFERENCE: 017753-091
CURRENT APPLICATION NUMBER: US/09/099,333A
CURRENT FILING DATE: 1998-06-18
EARLIER APPLICATION NUMBER: FR 93 14914
EARLIER FILING DATE: 1993-12-13
EARLIER APPLICATION NUMBER: US 08/215,248
EARLIER FILING DATE: 1994-03-21
EARLIER APPLICATION NUMBER: US 08/505,210
EARLIER FILING DATE: 1995-08-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 116
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-099-333-2

Query Match 98.8%; Score 338; DB 3; Length 116;
Best Local Similarity 98.5%; Pred. No. 3.5e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 50 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 109
QY 61 LESGTKE 67
DB 110 LESGTKE 116

RESULT 5
US-09-309-572-21
Sequence 21, Application US/09309572
Patent No. 6440730
GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 116
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
OTHER INFORMATION: rev protein
US-09-309-572-21

Query Match 98.8%; Score 338; DB 4; Length 116;
Best Local Similarity 98.5%; Pred. No. 3.5e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 50 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 109
QY 61 LESGTKE 67
DB 110 LESGTKE 116

RESULT 6
US-09-718-096-21
Sequence 21, Application US/09718096
Patent No. 6589763
GENERAL INFORMATION:

APPLICANT: Von Laer, Melke-Dorothee
TITLE OF INVENTION: RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
FILE REFERENCE: 35-195
CURRENT APPLICATION NUMBER: US/09/718,096
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: DE 19856463.5
PRIOR FILING DATE: 1998-11-26
PRIOR APPLICATION NUMBER: EP 99250415.9
PRIOR FILING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: US 09/309,572
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21
LENGTH: 116
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
OTHER INFORMATION: rev protein
US-09-718-096-21

Query Match 98.8%; Score 338; DB 4; Length 116;
Best Local Similarity 98.5%; Pred. No. 3.5e-34;
Matches 66; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 50 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 109
QY 61 LESGTKE 67
DB 110 LESGTKE 116

RESULT 7
US-09-124-900-7
Sequence 7, Application US/09124900
Patent No. 6268484
GENERAL INFORMATION:
APPLICANT: KATINSER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: ERNST, Wolfgang
APPLICANT: BALLAUN, Claudia
APPLICANT: PUDTSCHER, Martin
APPLICANT: TKOLA, Alexandra
APPLICANT: PREDL, Renate
APPLICANT: SCHWARTZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: STEINDL, Franz
APPLICANT: MISTER, Thomas
TITLE OF INVENTION: HIV-Vaccines
FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR FILING DATE: 1995-04-19
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 116
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-7

Query Match 97.4%; Score 333; DB 3; Length 116;
Best Local Similarity 97.0%; Pred. No. 1.4e-33;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 60
DB 50 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVGSPQIIVESPAY 109
QY 61 LESGTKE 67

Db 110 LESGAKE 116

RESULT 8
US-07-808-452-6

Sequence 6, Application US/07808452
Patent No. 6063612
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/808,452
FILING DATE: 19911213
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8255-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: the sequence of the REV protein of
US-07-808-452-6

Query Match 97.1%; Score 332; DB 3; Length 116;
Best Local Similarity 95.5%; Pred. No. 1.9e-33;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RQHSISRILSTYIGSAEVPQLPPLRLTLDNCNEDCGTSGTGVSGPQILVESPAV 60
DB 50 RQHSISRILSTYIGSAEVPQLPPLRLTLDNCNEDCGTSGTGVSGPQILVESPTI 109
QY 61 LESGKE 67
DB 110 LESGAKE 116

RESULT 9

PCT-US92-10770-6
Sequence 6, Application PC/TUS9210770
GENERAL INFORMATION:
APPLICANT: Jayasena, Sumedha D.
APPLICANT: Johnston, Brian H.
TITLE OF INVENTION: Antiviral Reagents Based on
RNA-Binding Proteins
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSEE: SRI International
STREET: 333 Ravenswood Avenue
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10770
FILING DATE: 19921211
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,452
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: P-2962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 859-3880
TELEFAX: (415) 859-4550
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 116 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: the sequence of the REV protein of
PCT-US92-10770-6

Query Match 97.1%; Score 332; DB 5; Length 116;
Best Local Similarity 95.5%; Pred. No. 1.9e-33;
Matches 64; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RQHSISRILSTYIGSAEVPQLPPLRLTLDNCNEDCGTSGTGVSGPQILVESPAV 60
DB 50 RQHSISRILSTYIGSAEVPQLPPLRLTLDNCNEDCGTSGTGVSGPQILVESPTI 109
QY 61 LESGKE 67
DB 110 LESGAKE 116

RESULT 10
US-08-488-551B-640

Sequence 640, Application US/08488551B
Patent No. 601561
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 640:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-551B-640

Query Match 87.7%; Score 300; DB 3; Length 94;
Best Local Similarity 86.6%; Pred. No. 1.3e-29;
Matches 58; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDCNEDCGTSGTQGVGSPQILVESP AV 60
Db 25 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDCNEDCGTSGTQGVGSPQILVESP AV 84
Qy 61 LESTGKE 67
Db 85 LEAGTTE 91

RESULT 11
US-08-388-353-640
Sequence 640, Application US/08388353
Patent No. 6010895
GENERAL INFORMATION:
APPLICANT: Deacon, Nicholas J.
APPLICANT: Learmont, Jennifer C.
APPLICANT: McPhee, Dale A.
APPLICANT: Crowe, Suzanne
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 800
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 640:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-388-353-640

Query Match 87.7%; Score 300; DB 3; Length 107;
Best Local Similarity 86.6%; Pred. No. 1.5e-29;
Matches 58; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDCNEDCGTSGTQGVGSPQILVESP AV 60
Db 25 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDCNEDCGTSGTQGVGSPQILVESP AV 84
Qy 61 LESTGKE 67
Db 85 LEAGTTE 91

RESULT 12
US-08-488-551B-639
Sequence 639, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 639:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-551B-639

Query Match 84.2%; Score 288; DB 3; Length 105;
Best Local Similarity 83.6%; Pred. No. 4, 5e-28;
Matches 56; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQGVGSPQIIVESPAV 60
DB 25 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQGVGSPQIIVESPAV 84

QY 61 LESGTKE 67
DB 85 LEPGTAE 91

RESULT 13

US-08-388-353-639

Sequence 639, Application US/08388353

Patent No. 6010895

GENERAL INFORMATION:

APPLICANT: Deacon, Nicholas J.

APPLICANT: Leamont, Jennifer C.

APPLICANT: McPhee, Dale A.

APPLICANT: Crowe, Suzanne

APPLICANT: Cooper, David

TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

NUMBER OF SEQUENCES: 800

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: DiGiullo, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4366

TELEFAX: (516) 742-4343

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 639:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-388-353-639

Query Match 84.2%; Score 288; DB 3; Length 108;
Best Local Similarity 83.6%; Pred. No. 4, 7e-28;
Matches 56; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQGVGSPQIIVESPAV 60
DB 25 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQGVGSPQIIVESPAV 84

QY 61 LESGTKE 67

DB 85 LEPGTAE 91

RESULT 14

US-09-319-588C-16

Sequence 16, Application US/09319588C

Patent No. 6509018

GENERAL INFORMATION:

APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE-INSERM

APPLICANT: ASSISTANCE PUBLIQUE-HOPITAUX DE PARIS

APPLICANT: INSTITUT PASTEUR

APPLICANT: MAUCIERE, Philippe

APPLICANT: LOUSSEY-ADAKA, Idtiseam

APPLICANT: SIMON, Francois

APPLICANT: SARAGOSTI, Sentob

APPLICANT: BARRE-SINOUSSI, Francoise

TITLE OF INVENTION: NON-M NON-O HIV STRAINS, FRAGMENTS AND APPLICATIONS.

FILE REFERENCE: 5980512

CURRENT APPLICATION NUMBER: US/09/319,588C

CURRENT FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: FR96/15087

PRIOR FILING DATE: 1996-12-09

NUMBER OF SEQ ID NOS: 98

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 16

LENGTH: 103

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-319-588C-16

Query Match 43.3%; Score 148; DB 4; Length 103;
Best Local Similarity 67.4%; Pred. No. 8, 2e-11;
Matches 31; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQ 46
DB 49 RQHSISIRIISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQ 94

RESULT 15

US-09-337-387-12

Sequence 12, Application US/09337387

Patent No. 6420545

GENERAL INFORMATION:

APPLICANT: HOXIE, James A.

APPLICANT: LABRANCHE, Celia C.

APPLICANT: DOMS, Robert W.

APPLICANT: HOFFMAN, Trevor L.

TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND

FILE REFERENCE: Hoxie 9596-10401 (0282)

CURRENT APPLICATION NUMBER: US/09/337,387

CURRENT FILING DATE: 1999-06-22

PRIOR APPLICATION NUMBER: US 09/317,556

PRIOR FILING DATE: 1999-05-24

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 759

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-337-387-12

Query Match 42.1%; Score 144; DB 4; Length 759;
Best Local Similarity 85.3%; Pred. No. 2, 9e-09;
Matches 29; Conservative 3; Mismatches 0; Indels 2; Gaps 1;

QY 8 ERLISTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQ 39
DB 726 KRLINTYIGRSABVPVLPPLPRLTLDNCNDCGSGTQ 759

Search completed: December 14, 2004, 16:43:00

Tue Dec 14 17:05:13 2004

Job time : 46.225 secs

us-09-055-744a-9.ra1

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 167.5 Seconds
(without alignments)
142.871 Million cell updates/sec

Title: US-09-055-744a-9

Perfect score: 342
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Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
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Post-processing: Minimum Match 100%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	321	93.9	65	US-09-055-744-9	Sequence 9, Appl
4	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
5	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
6	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
7	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
8	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
9	309	90.4	419	US-10-138-098-46	Sequence 25, Appl
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41 <td>207.5 <td>60.7 <td>124 <td>14 <td>US-10-190-435-249</td> <td>Sequence 249, App</td> </td></td></td></td>	207.5 <td>60.7 <td>124 <td>14 <td>US-10-190-435-249</td> <td>Sequence 249, App</td> </td></td></td>	60.7 <td>124 <td>14 <td>US-10-190-435-249</td> <td>Sequence 249, App</td> </td></td>	124 <td>14 <td>US-10-190-435-249</td> <td>Sequence 249, App</td> </td>	14 <td>US-10-190-435-249</td> <td>Sequence 249, App</td>	US-10-190-435-249	Sequence 249, App
42 <td>207.5 <td>60.7 <td>126 <td>14 <td>US-10-190-435-238</td> <td>Sequence 238, App</td> </td></td></td></td>	207.5 <td>60.7 <td>126 <td>14 <td>US-10-190-435-238</td> <td>Sequence 238, App</td> </td></td></td>	60.7 <td>126 <td>14 <td>US-10-190-435-238</td> <td>Sequence 238, App</td> </td></td>	126 <td>14 <td>US-10-190-435-238</td> <td>Sequence 238, App</td> </td>	14 <td>US-10-190-435-238</td> <td>Sequence 238, App</td>	US-10-190-435-238	Sequence 238, App
43 <td>205.5 <td>60.1 <td>126 <td>14 <td>US-10-190-435-231</td> <td>Sequence 231, App</td> </td></td></td></td>	205.5 <td>60.1 <td>126 <td>14 <td>US-10-190-435-231</td> <td>Sequence 231, App</td> </td></td></td>	60.1 <td>126 <td>14 <td>US-10-190-435-231</td> <td>Sequence 231, App</td> </td></td>	126 <td>14 <td>US-10-190-435-231</td> <td>Sequence 231, App</td> </td>	14 <td>US-10-190-435-231</td> <td>Sequence 231, App</td>	US-10-190-435-231	Sequence 231, App
44 <td>204.5 <td>59.8 <td>107 <td>15 <td>US-10-296-734-1482</td> <td>Sequence 1482, Ap</td> </td></td></td></td>	204.5 <td>59.8 <td>107 <td>15 <td>US-10-296-734-1482</td> <td>Sequence 1482, Ap</td> </td></td></td>	59.8 <td>107 <td>15 <td>US-10-296-734-1482</td> <td>Sequence 1482, Ap</td> </td></td>	107 <td>15 <td>US-10-296-734-1482</td> <td>Sequence 1482, Ap</td> </td>	15 <td>US-10-296-734-1482</td> <td>Sequence 1482, Ap</td>	US-10-296-734-1482	Sequence 1482, Ap
45 <td>204.5 <td>59.8 <td>124 <td>14 <td>US-10-190-435-244</td> <td>Sequence 244, App</td> </td></td></td></td>	204.5 <td>59.8 <td>124 <td>14 <td>US-10-190-435-244</td> <td>Sequence 244, App</td> </td></td></td>	59.8 <td>124 <td>14 <td>US-10-190-435-244</td> <td>Sequence 244, App</td> </td></td>	124 <td>14 <td>US-10-190-435-244</td> <td>Sequence 244, App</td> </td>	14 <td>US-10-190-435-244</td> <td>Sequence 244, App</td>	US-10-190-435-244	Sequence 244, App

ALIGNMENTS

RESULT 1
US-10-190-435-252
Sequence 252, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDR, Jan W.
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBOURG, Estrelita J.
TITLE OF INVENTION: POLYPEPTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 252
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rev HXB2
US-10-190-435-252

Query Match	97.7%	Score 334	DB 14	Length 116
Best Local Similarity	97.0%	Pred. No. 1.5e-32		
Matches	65	Conservative	0	Mismatches 2; Indels 0; Gaps 0;
1	RQHSISERILSTYLSGRSAEVPPLPLRLTLDCNEDCGTSGTGVGSPQLVSPAV	60		
50	RQHSISERILSTYLSGRSAEVPPLPLRLTLDCNEDCGTSGTGVGSPQLVSPAV	109		
61	LESSTKE 67			
110	LESSTKE 116			

```
RESULT 2
US-10-093-953A-49
; Sequence 49, Application US/10093953A
; Publication No. US20040105871A1
GENERAL INFORMATION:
; APPLICANT: Robinson, Harriet L.
; APPLICANT: Smith, James M.
; APPLICANT: Hua, Jian
; APPLICANT: Mose, Bernard
; APPLICANT: Amara, Rama
; APPLICANT: Wyatt, Linda
; APPLICANT: Earl, Patricia
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENERATING
; FILE REFERENCE: 12804-005002
CURRENT APPLICATION NUMBER: US/10/093,953A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 60/186,364
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/251,083
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/798,675
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: PCT/US01/06795
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: US 60/324,845
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/325,004
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 81
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: protein encoded by construct of vaccine vector
; OTHER INFORMATION: pgal and vaccine insert expressing clade B HIV-1
; OTHER INFORMATION: Gag-Pol
US-10-093-953A-49

Query Match          97.4%; Score 333; DB 16; Length 81;
Best Local Similarity 97.0%; Pred. No. 1.3e-32;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPAV 60
Db 15 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPTV 74

Qy 61 LESGTXE 67
Db 75 LESGTXE 81

RESULT 3
US-09-055-744-9
; Sequence 9, Application US/09055744
; Publication No. US20010019714A1
GENERAL INFORMATION:
; APPLICANT: Sia, Charles
; APPLICANT: Chong, Pele
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: HIV-SPECIFIC CYTOTOXIC T-CELL RESPONSES
; FILE REFERENCE: 1038-746
CURRENT APPLICATION NUMBER: US/09/055,744
CURRENT FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 65
TYPE: PRT
```

```
; ORGANISM: Human immunodeficiency virus type 1
US-09-055-744-9

Query Match          93.9%; Score 321; DB 9; Length 65;
Best Local Similarity 97.0%; Pred. No. 2.8e-31;
Matches 65; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPAV 60
Db 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPAV 58

Qy 61 LESGTXE 67
Db 59 LESGTXE 65

RESULT 4
US-10-138-098-25
; Sequence 25, Application US/10138098
; Publication No. US20030129169A1
GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna
; APPLICANT: Tahtinen, Marja
; APPLICANT: Ustlav, Mart
; APPLICANT: Toole, Urvie
; APPLICANT: Mannik, Andres
; APPLICANT: Ranki, Annamari
; APPLICANT: Sikut, Rein
; APPLICANT: Janikson, Kadri
; APPLICANT: Ustlav, Ene
; TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
; FILE REFERENCE: 11041-006-999
CURRENT APPLICATION NUMBER: US/10/138,098
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FI 20010922
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 419
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Hybrid protein comprised of Nef-Tat-Rev (NTR)
US-10-138-098-25

Query Match          90.4%; Score 309; DB 14; Length 419;
Best Local Similarity 89.6%; Pred. No. 7.9e-29;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPAV 60
Db 251 RQHSISRILSTYLGSAEPVPLQLPPLRLTLDNCNEDCGTSGTGVSPOILVESPAV 310

Qy 61 LESGTXE 67
Db 311 LESGTXE 317

RESULT 5
US-10-138-098-26
; Sequence 26, Application US/10138098
; Publication No. US20030129169A1
GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna
; APPLICANT: Tahtinen, Marja
; APPLICANT: Ustlav, Mart
; APPLICANT: Toole, Urvie
; APPLICANT: Mannik, Andres
; APPLICANT: Ranki, Annamari
; APPLICANT: Sikut, Rein
```

```

: APPLICANT: Janikson, Kadri
: APPLICANT: Ustlav, Ene
: TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
: FILE REFERENCE: 11041-006-999
: CURRENT APPLICATION NUMBER: US/10/138,098
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: FI 20010922
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 26
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Hybrid protein comprised of Tat-Rev-Nef (TRN)
US-10-138-098-26

Query Match          90.4%; Score 309; DB 14; Length 419;
Best Local Similarity 89.6%; Pred. No. 7.9e-29;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 60
DB 152 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 211
      |||||
QY 61 LESGTYE 67
DB 212 LEPGTYE 218

RESULT 6
US-10-138-098-27
: Sequence 27, Application US/10138098
: Publication No. US20030129169A1
: GENERAL INFORMATION:
: APPLICANT: Krohn, Kai
: APPLICANT: Blazevic, Vesna
: APPLICANT: Tahminen, Marja
: APPLICANT: Ustlav, Mart
: APPLICANT: Toots, Urve
: APPLICANT: Mannik, Andres
: APPLICANT: Ranki, Annamari
: APPLICANT: Sikut, Rein
: APPLICANT: Janikson, Kadri
: APPLICANT: Ustlav, Ene
: TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
: FILE REFERENCE: 11041-006-999
: CURRENT APPLICATION NUMBER: US/10/138,098
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: FI 20010922
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 27
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Hybrid protein comprised of Rev-Tat-Nef (RTN)
US-10-138-098-27

Query Match          90.4%; Score 309; DB 14; Length 419;
Best Local Similarity 89.6%; Pred. No. 7.9e-29;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 60
DB 50 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 109
      |||||
QY 61 LESGTYE 67
DB 110 LEPGTYE 116
```

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RESULT 7
US-10-138-098-28
: Sequence 28, Application US/10138098
: Publication No. US20030129169A1
: GENERAL INFORMATION:
: APPLICANT: Krohn, Kai
: APPLICANT: Blazevic, Vesna
: APPLICANT: Tahminen, Marja
: APPLICANT: Ustlav, Mart
: APPLICANT: Toots, Urve
: APPLICANT: Mannik, Andres
: APPLICANT: Ranki, Annamari
: APPLICANT: Sikut, Rein
: APPLICANT: Janikson, Kadri
: APPLICANT: Ustlav, Ene
: TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
: FILE REFERENCE: 11041-006-999
: CURRENT APPLICATION NUMBER: US/10/138,098
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: FI 20010922
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 28
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Hybrid protein comprised of Tat-Nef-Rev (TNR)
US-10-138-098-28

Query Match          90.4%; Score 309; DB 14; Length 419;
Best Local Similarity 89.6%; Pred. No. 7.9e-29;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 60
DB 353 ROHSISRIISTYLGSAEPVPLQLPPLERLTLDNCNEDCGTSGTGVSPOILVESPAV 412
      |||||
QY 61 LESGTYE 67
DB 413 LEPGTYE 419

RESULT 8
US-10-138-098-29
: Sequence 29, Application US/10138098
: Publication No. US20030129169A1
: GENERAL INFORMATION:
: APPLICANT: Krohn, Kai
: APPLICANT: Blazevic, Vesna
: APPLICANT: Tahminen, Marja
: APPLICANT: Ustlav, Mart
: APPLICANT: Toots, Urve
: APPLICANT: Mannik, Andres
: APPLICANT: Ranki, Annamari
: APPLICANT: Sikut, Rein
: APPLICANT: Janikson, Kadri
: APPLICANT: Ustlav, Ene
: TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
: FILE REFERENCE: 11041-006-999
: CURRENT APPLICATION NUMBER: US/10/138,098
: PRIOR FILING DATE: 2002-05-03
: PRIOR APPLICATION NUMBER: FI 20010922
: PRIOR FILING DATE: 2001-05-03
: NUMBER OF SEQ ID NOS: 52
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 29
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Artificial Sequence
```


Db 212 LEPTKE 218

RESULT 12

US-10-138-098-45
; Sequence 45, Application US/10138098
; Publication No. US20030129169A1
; GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna
; APPLICANT: Tahminen, Marja
; APPLICANT: Ustev, Mart
; APPLICANT: Toots, Urve
; APPLICANT: Mannik, Andres
; APPLICANT: Ranki, Annamari
; APPLICANT: Sikut, Rein
; APPLICANT: Janikson, Kadri
; APPLICANT: Ustev, Ene
; TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
; FILE REFERENCE: 11041-006-999
; CURRENT APPLICATION NUMBER: US/10/138,098
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FI 20010922
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid protein cds comprised of Tat-Rev-Nef, truncated Gag protei
; OTHER INFORMATION: and CTL(TRN-optp17/24-CTL)
US-10-138-098-45

Query Match 90.4%; Score 309; DB 14; Length 1006;
Best Local Similarity 89.6%; Pred. No. 2.3e-28;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 60
Db 152 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 211

Qy 61 LEPTKE 67
Db 212 LEPTKE 218

RESULT 13

US-10-138-098-46
; Sequence 46, Application US/10138098
; Publication No. US20030129169A1
; GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna
; APPLICANT: Tahminen, Marja
; APPLICANT: Ustev, Mart
; APPLICANT: Toots, Urve
; APPLICANT: Mannik, Andres
; APPLICANT: Ranki, Annamari
; APPLICANT: Sikut, Rein
; APPLICANT: Janikson, Kadri
; APPLICANT: Ustev, Ene
; TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
; FILE REFERENCE: 11041-006-999
; CURRENT APPLICATION NUMBER: US/10/138,098
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FI 20010922
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46

; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid protein cdscomprised of Tat-Rev-Nef, CTL and truncated Gag
; OTHER INFORMATION: protein (TRN-CTL-optp17/24)
US-10-138-098-46

Query Match 90.4%; Score 309; DB 14; Length 1006;
Best Local Similarity 89.6%; Pred. No. 2.3e-28;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 60
Db 152 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 211

Qy 61 LEPTKE 67
Db 212 LEPTKE 218

RESULT 14

US-10-138-098-47
; Sequence 47, Application US/10138098
; Publication No. US20030129169A1
; GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna
; APPLICANT: Tahminen, Marja
; APPLICANT: Ustev, Mart
; APPLICANT: Toots, Urve
; APPLICANT: Mannik, Andres
; APPLICANT: Ranki, Annamari
; APPLICANT: Sikut, Rein
; APPLICANT: Janikson, Kadri
; APPLICANT: Ustev, Ene
; TITLE OF INVENTION: No. US20030129169A1 expression vectors and uses thereof
; FILE REFERENCE: 11041-006-999
; CURRENT APPLICATION NUMBER: US/10/138,098
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FI 20010922
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid protein comprised of Rev-Nef-Tat, CTL and truncated Gag
; OTHER INFORMATION: protein (RNT-CTL-optp17/24)
US-10-138-098-47

Query Match 90.4%; Score 309; DB 14; Length 1006;
Best Local Similarity 89.6%; Pred. No. 2.3e-28;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 60
Db 50 RQHSISERILSTYLGSAEPVPLQLPPLERLTLDNCNDCGSGTGQVGSFQILVESPAV 109

Qy 61 LEPTKE 67
Db 110 LEPTKE 116

RESULT 15

US-10-138-098-48
; Sequence 48, Application US/10138098
; Publication No. US20030129169A1
; GENERAL INFORMATION:
; APPLICANT: Krohn, Kai
; APPLICANT: Blazevic, Vesna

APPLICANT: Tahtinen, Maria
APPLICANT: Uteav, Mart
APPLICANT: Toote, Urve
APPLICANT: Mannik, Andres
APPLICANT: Ranki, Annamari
APPLICANT: Sikut, Rein
APPLICANT: Jankson, Kadri
APPLICANT: Uteav, Ene
TITLE OF INVENTION: No. US20030129169A1e1 expression vectors and uses thereof
FILE REFERENCE: 11041-006-999
CURRENT APPLICATION NUMBER: US/10/138,098
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FI 20010922
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
LENGTH: 1006
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hybrid protein comprised of Rev-Nef-Tat, truncated Gag protein an
US-10-138-098-48

Query Match 90.4%; Score 309; DB 14; Length 1006;
Best Local Similarity 89.6%; Pred. No. 2.3e-28;
Matches 60; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQHSISERISTYIGRSAPVPLQLPPLERLTLDPCNEDCGTSGTQGVSPQIIVESPAV 60
DB 50 RQHSISERISTYIGRSAPVPLQLPPLERLTLDPCNEDCGTSGTQGVSPQIIVESPAV 109
QY 61 LESGTKE 67
DB 110 LESGTKE 116

Search completed: December 14, 2004, 16:51:39
Job time : 167.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 7.6375 Seconds
(without alignments)
163.773 Million cell updates/sec

Title: US-09-055-744A-10
Perfect score: 74
Sequence: 1-TPPAYRPPNAPIL 13

Scoring table: BIOSUM62
Gapop-10-0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	183	1 NKVLA2	core antigen - hep
2	74	100.0	183	1 NKVLCF	core antigen - hep
3	74	100.0	183	2 S53181	core antigen - hep
4	74	100.0	183	2 S53260	core antigen - hep
5	74	100.0	183	2 S53214	core antigen - hep
6	74	100.0	183	2 S53175	core antigen - hep
7	74	100.0	183	2 S53152	core antigen - hep
8	74	100.0	183	2 S53221	core antigen - hep
9	74	100.0	183	2 S53140	core antigen - hep
10	74	100.0	183	2 S53232	core antigen - hep
11	74	100.0	183	2 S20755	core antigen - hep
12	74	100.0	183	2 S53172	core antigen - hep
13	74	100.0	183	2 S53166	core antigen - hep
14	74	100.0	183	2 S53129	core antigen - hep
15	74	100.0	183	2 S53189	core antigen - hep
16	74	100.0	183	2 S53186	core antigen - hep
17	74	100.0	183	2 S53169	core antigen - hep
18	74	100.0	183	2 S53194	core antigen - hep
19	74	100.0	183	2 S53270	core antigen - hep
20	74	100.0	183	2 S53247	core antigen - hep
21	74	100.0	184	2 S53146	core antigen - hep
22	74	100.0	195	1 NKVLA3	core antigen - hep
23	74	100.0	211	1 NKVLA4	e antigen precursor
24	74	100.0	212	1 NKVLA1	e antigen precursor
25	74	100.0	212	1 NKVLAH	e antigen precursor
26	74	100.0	212	1 NKVLAH	e antigen precursor
27	74	100.0	212	1 NKVLAJ1	e antigen precursor
28	74	100.0	212	1 NKVLAJ2	e antigen precursor
29	74	100.0	212	2 S53238	e antigen precursor

30	74	100.0	212	2 S53227	e antigen precursor
31	74	100.0	212	2 S67504	e antigen precursor
32	74	100.0	212	2 S53281	e antigen precursor
33	74	100.0	212	2 S53240	e antigen precursor
34	74	100.0	212	2 S53272	e antigen precursor
35	74	100.0	212	2 S53229	e antigen precursor
36	74	100.0	212	2 S53202	e antigen precursor
37	74	100.0	212	2 S53163	e antigen precursor
38	74	100.0	212	2 S53216	e antigen precursor
39	74	100.0	212	2 S53257	e antigen precursor
40	74	100.0	212	2 S53255	e antigen precursor
41	74	100.0	212	2 S20746	e antigen precursor
42	74	100.0	212	2 S20750	e antigen precursor
43	74	100.0	212	2 S53236	e antigen precursor
44	74	100.0	212	2 S32204	e antigen precursor
45	74	100.0	212	2 S53204	e antigen precursor

ALIGNMENTS

RESULT 1

NKVLA2
core antigen - hepatitis B virus (subtype adyw)

C:Species: hepatitis B virus, HBV

A:Variety: subtype adyw

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: B93217, A03711

R:Pasak, W.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; Mackay, P.; Leadbetter, G.;

Nature 282, 575-579, 1979

A:Title: Hepatitis B virus genes and their expression in E. coli.

A:Reference number: A93217, MUID:8102115, PMID:399329

A:Accession: B93217

A:Molecule type: DNA

A:Residues: 1-183 <PAS>

A:Cross-references: UNIPROT:P03147; GB:J02202; NID:G329637; PIDN:AAA45486.1; PID:G329638

A:Experimental source: subtype adyw

A>Note: due to a stop codon between the alternative initiators the e antigen precursor c

C:Genetics:

A:Gene: C

C:Superfamily: hepatitis B virus core antigen

C:Keywords: core protein

F.1-183/Product: core antigen #status predicted <MAT>

Query Match	100.0%	Score 74;	DB 1;	Length 183;
Best Local Similarity	100.0%	Pred. NO. 0.0067;		
Matches 13; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TPPAYRPPNAPIL 13		
Db	128	TPPAYRPPNAPIL 140		

RESULT 2

NKVLCF
core antigen - hepatitis B virus (strain LSH, chimpanzee)

C:Species: hepatitis B virus, HBV

A:Variety: strain LSH, chimpanzee

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C:Accession: A28885

J. Vandin, M.; Wolstenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.

J. Gen. Virol. 69, 1383-1389, 1988

A:Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated.

A:Reference number: A92796; MUID:86258473; PMID:2838576

A:Accession: A28885

A:Molecule type: DNA

A:Residues: 1-183 <VAU>

A:Cross-references: UNIPROT:P12901; EMBL:D00220; NID:G221505; PIDN:BA00157.1; PID:G2215

A:Experimental source: strain LSH, chimpanzee

A>Note: due to a stop codon between the alternative initiators the e antigen precursor c

C:Genetics:

A:Gene: C

C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 100.0%; Score 74; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 3

S53181
core antigen - hepatitis B virus
N;Alternate names: HBC antigen
N;Contains: core antigen

C;Species: hepatitis B virus, HBV

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: S53181; S53291
R;Lat, M.E.; Mazzelet, A.P.; Portu, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53181

A;Molecule type: DNA

A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67997; EMBL:X85279; NID:G736073; PIDN:CAAS9583.1; PID:G7360

A;Experimental source: isolate patient Bicti'89

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

A;Accession: S53291

A;Molecule type: DNA

A;Residues: 1-20, 'T', '22-37, 'L', '39, 'D', '41-57, 'E', '59-76, 'Q', '78-83, 'L', '85-86, 'N', '88-146, 'S'

A;Cross-references: EMBL:X85263; NID:G736232; PIDN:CAAS9538.1; PID:G736235

A;Experimental source: isolate patient Amoroso'89

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 4
S53260
core antigen - hepatitis B virus (isolate patient Mannoni-3'94)

N;Alternate names: HBC antigen
N;Contains: core antigen

C;Species: hepatitis B virus, HBV

A;Variety: isolate patient Mannoni-3'94

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: S53260
R;Lat, M.E.; Mazzelet, A.P.; Portu, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53260

A;Molecule type: DNA

A;Residues: 1-183 <LAI>

A;Cross-references: UNIPROT:Q68060; EMBL:X85311; NID:G736187; PIDN:CAAS9655.1; PID:G7361

A;Experimental source: isolate patient Mannoni-3'94

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: core protein

Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 5
S53214
core antigen - hepatitis B virus (isolate patient Castag-2'86)

N;Alternate names: HBC antigen
N;Contains: core antigen

C;Species: hepatitis B virus, HBV

A;Variety: isolate patient Castag-2'86

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: S53214

R;Lat, M.E.; Mazzelet, A.P.; Portu, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53214

A;Molecule type: DNA

A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68023; EMBL:X85292; NID:G736120; PIDN:CAAS9614.1; PID:G73612

A;Experimental source: isolate patient Castag-2'86

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 6
S53175
core antigen - hepatitis B virus (isolate patient Boi'90)

N;Alternate names: HBC antigen
N;Contains: core antigen

C;Species: hepatitis B virus, HBV

A;Variety: isolate patient Boi'90

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

C;Accession: S53175

R;Lat, M.E.; Mazzelet, A.P.; Portu, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995

A;Reference number: S53112

A;Accession: S53175

A;Molecule type: DNA

A;Residues: 1-183 <LAI>

A;Cross-references: UNIPROT:Q67993; EMBL:X85277; NID:G736065; PIDN:CAAS9577.1; PID:G73606

A;Experimental source: isolate patient Boi'90

A;Note: due to a stop codon between the alternative initiators the e antigen precursor

C;Genetics:

A;Gene: C

C;Superfamily: hepatitis B virus core antigen

C;Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 128 TPPAYRPPNAPIL 140

RESULT 7

553152
 core antigen - hepatitis B virus (isolate patient Tufariello'89)
 N/Alternate names: HBC antigen
 N/Contains: core antigen
 C/Species: hepatitis B virus, HBV
 A/Variety: isolate patient Tufariello'89
 C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S53152
 R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A/Reference number: S53112
 A/Accession: S53152
 A/Molecule type: DNA
 A/Residues: 1-183 <LAI>
 A/Cross-references: UNIPROT:Q67973; EMBL:X85269; NID:G736033; PIDN:CAA59556.1; PID:G7360
 A/Experimental source: isolate patient Tufariello'89
 A/Note: due to a stop codon between the alternative initiators the e antigen precursor
 C/Genetics:
 A/Gene: C
 C/Superfamily: hepatitis B virus core antigen
 C/Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
 |||||
 Db 128 TTPAYRPPNAPIL 140

RESULT 8
 S53221
 core antigen - hepatitis B virus (isolate patient Giulioc'92)
 N/Alternate names: HBC antigen
 N/Contains: core antigen
 C/Species: hepatitis B virus, HBV
 A/Variety: isolate patient Giulioc'92
 C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S53221
 R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A/Reference number: S53112
 A/Accession: S53221
 A/Molecule type: DNA
 A/Residues: 1-183 <LAI>
 A/Cross-references: UNIPROT:Q68027; EMBL:X85258; NID:G736127; PIDN:CAA59525.1; PID:G7361
 A/Experimental source: isolate patient Giulioc'92
 A/Note: due to a stop codon between the alternative initiators the e antigen precursor
 C/Genetics:
 A/Gene: C
 C/Superfamily: hepatitis B virus core antigen
 C/Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
 |||||
 Db 128 TTPAYRPPNAPIL 140

RESULT 9
 S53140
 core antigen - hepatitis B virus (isolate patient Fraills'92)
 N/Alternate names: HBC antigen
 N/Contains: core antigen
 C/Species: hepatitis B virus, HBV
 A/Variety: isolate patient Fraills'92
 C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S53140
 R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995
 A/Reference number: S53112
 A/Accession: S53140
 A/Molecule type: DNA
 A/Residues: 1-183 <LAI>
 A/Cross-references: UNIPROT:Q67964; EMBL:X85265; NID:G736017; PIDN:CAA59544.1; PID:G7360
 A/Experimental source: isolate patient Fraills'92
 A/Note: due to a stop codon between the alternative initiators the e antigen precursor
 C/Genetics:
 A/Gene: C
 C/Superfamily: hepatitis B virus core antigen
 C/Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
 |||||
 Db 128 TTPAYRPPNAPIL 140

RESULT 10
 S53232
 core antigen - hepatitis B virus (isolate patient Dettori-2'87)
 N/Alternate names: HBC antigen
 N/Contains: core antigen
 C/Species: hepatitis B virus, HBV
 A/Variety: isolate patient Dettori-2'87
 C/Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C/Accession: S53232
 R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A/Reference number: S53112
 A/Accession: S53232
 A/Molecule type: DNA
 A/Residues: 1-183 <LAI>
 A/Cross-references: UNIPROT:Q68037; EMBL:X85299; NID:G736146; PIDN:CAA59629.1; PID:G7361
 A/Experimental source: isolate patient Dettori-2'87
 A/Note: due to a stop codon between the alternative initiators the e antigen precursor
 C/Genetics:
 A/Gene: C
 C/Superfamily: hepatitis B virus core antigen
 C/Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
 |||||
 Db 128 TTPAYRPPNAPIL 140

RESULT 11
 S20755
 core antigen - hepatitis B virus
 N/Alternate names: HBC antigen
 N/Contains: core antigen
 C/Species: hepatitis B virus, HBV
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: S20755; S53134
 R/Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Mells, A.; Porru, A.
 submitted to the EMBL Data Library, March 1992
 A/Description: Sequence analysis of HBV genomes isolated from patients with HBsAg negati
 A/Reference number: S20745
 A/Accession: S20755
 A/Molecule type: DNA
 A/Residues: 1-183 <LAI>
 A/Cross-references: UNIPROT:Q67880; EMBL:X65259; NID:G59439; PIDN:CAA46359.1; PID:G59442
 A/Experimental source: subtype ayw, patient B
 A/Note: due to a stop codon between the alternative initiators the e antigen precursor
 R/Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Accession: S53112
 A:Molecule type: DNA
 A:Residues: 1-7, 'E', '9-11', 'S', '13-16', 'SF', '19-24', 'PS', '27-33', 'S', '35-37', 'E', '39', 'D', '41-48', 'T',
 A:Cross-references: EMBL:X85255, NID:g736009, PIDN:CA59517.1, PID:g736012
 A:Experimental source: isolate patient Tarcisloc.92
 A>Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPAYRPPNAPIL 13
 |||||
 Db 128 TPAYRPPNAPIL 140

RESULT 12
 S53172
 core antigen - hepatitis B virus (isolate patient Urtis'89)
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Urtis'89
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C:Accession: S53172
 R:Lat, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Residues: 1-183 <LAI>
 A:Cross-references: UNIPROT:Q67991; EMBL:X85276, NID:g736061, PIDN:CA59574.1, PID:g7360
 A:Experimental source: isolate patient Urtis'89
 A>Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPAYRPPNAPIL 13
 |||||
 Db 128 TPAYRPPNAPIL 140

RESULT 13
 S53166
 core antigen - hepatitis B virus (isolate patient Tedde'89)
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Tedde'89
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C:Accession: S53166
 R:Lat, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Accession: S53166
 A:Residues: 1-183 <LAI>
 A:Cross-references: UNIPROT:Q67986; EMBL:X85274, NID:g736053, PIDN:CA59568.1, PID:g7360
 A:Experimental source: isolate patient Tedde'89
 A>Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:

A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPAYRPPNAPIL 13
 |||||
 Db 128 TPAYRPPNAPIL 140

RESULT 14
 S53129
 core antigen - hepatitis B virus
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C:Accession: S53129
 R:Lat, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Residues: 1-183 <LAI>
 A:Cross-references: UNIPROT:Q67946; EMBL:X85254, NID:g736003, PIDN:CA59512.1, PID:g73600
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPAYRPPNAPIL 13
 |||||
 Db 128 TPAYRPPNAPIL 140

RESULT 15
 S53189
 core antigen - hepatitis B virus (isolate patient Serra'89)
 N:Alternate names: Hbc antigen
 N:Contains: core antigen
 C:Species: hepatitis B virus, HBV
 A:Variety: isolate patient Serra'89
 C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
 C:Accession: S53189
 R:Lat, M.E.; Mazzioleni, A.P.; Porru, A.; Balestrieri, A.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53112
 A:Molecule type: DNA
 A:Accession: S53189
 A:Residues: 1-183 <LAI>
 A:Cross-references: UNIPROT:Q68003; EMBL:X85282, NID:g736084, PIDN:CA59591.1, PID:g7360
 A:Experimental source: isolate patient Serra'89
 A>Note: due to a stop codon between the alternative initiators the e antigen precursor
 C:Genetics:
 A:Gene: C
 C:Superfamily: hepatitis B virus core antigen
 C:Keywords: core protein

Query Match 100.0%; Score 74; DB 2; Length 183;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPAYRPPNAPIL 13
 |||||
 Db 128 TPAYRPPNAPIL 140

Tue Dec 14 17:05:13 2004

us-09-055-744a-10.rpr

Page 5

Search completed: December 14, 2004, 16:43:55
Job time : 8.6375 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 41.275 Seconds

(without alignment)
181.220 Million cell updates/sec

Title: US-09-055-744A-10
Perfect score: 74
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	74	100.0	96 2 Q77BF4	Q77BF4 hepatitis b
2	74	100.0	96 2 Q77BF6	Q77BF6 hepatitis b
3	74	100.0	96 2 Q77BF8	Q77BF8 hepatitis b
4	74	100.0	96 2 Q77BG0	Q77BG0 hepatitis b
5	74	100.0	96 2 Q77BG1	Q77BG1 hepatitis b
6	74	100.0	96 2 Q77BG3	Q77BG3 hepatitis b
7	74	100.0	96 2 Q77BG4	Q77BG4 hepatitis b
8	74	100.0	96 2 Q77BG5	Q77BG5 hepatitis b
9	74	100.0	96 2 Q77BG7	Q77BG7 hepatitis b
10	74	100.0	96 2 Q77BG9	Q77BG9 hepatitis b
11	74	100.0	96 2 Q77BH1	Q77BH1 hepatitis b
12	74	100.0	96 2 Q77BH3	Q77BH3 hepatitis b
13	74	100.0	96 2 Q9YJM3	Q9YJM3 hepatitis b
14	74	100.0	96 2 Q9YJM4	Q9YJM4 hepatitis b
15	74	100.0	113 2 Q80J61	Q80J61 hepatitis b
16	74	100.0	130 2 Q8JSV0	Q8JSV0 hepatitis b
17	74	100.0	130 2 Q8JSV1	Q8JSV1 hepatitis b
18	74	100.0	130 2 Q8JSV2	Q8JSV2 hepatitis b
19	74	100.0	130 2 Q8JSV3	Q8JSV3 hepatitis b
20	74	100.0	130 2 Q8JSV4	Q8JSV4 hepatitis b
21	74	100.0	130 2 Q8JSV5	Q8JSV5 hepatitis b
22	74	100.0	130 2 Q8JSV6	Q8JSV6 hepatitis b
23	74	100.0	130 2 Q8JSV7	Q8JSV7 hepatitis b
24	74	100.0	130 2 Q8JSV9	Q8JSV9 hepatitis b
25	74	100.0	130 2 Q8JSM0	Q8JSM0 hepatitis b
26	74	100.0	130 2 Q8JSM1	Q8JSM1 hepatitis b
27	74	100.0	130 2 Q8JSM2	Q8JSM2 hepatitis b
28	74	100.0	130 2 Q8JSM3	Q8JSM3 hepatitis b
29	74	100.0	130 2 Q8JSM4	Q8JSM4 hepatitis b
30	74	100.0	130 2 Q8JSM5	Q8JSM5 hepatitis b
31	74	100.0	130 2 Q8JSM6	Q8JSM6 hepatitis b

32	74	100.0	130 2 Q8JSM7	Q8JSM7 hepatitis b
33	74	100.0	130 2 Q8JSM8	Q8JSM8 hepatitis b
34	74	100.0	130 2 Q8JSM9	Q8JSM9 hepatitis b
35	74	100.0	130 2 Q8JSM0	Q8JSM0 hepatitis b
36	74	100.0	130 2 Q8JSM1	Q8JSM1 hepatitis b
37	74	100.0	130 2 Q8JSM2	Q8JSM2 hepatitis b
38	74	100.0	130 2 Q8JSM3	Q8JSM3 hepatitis b
39	74	100.0	130 2 Q8JSM4	Q8JSM4 hepatitis b
40	74	100.0	130 2 Q8JSM5	Q8JSM5 hepatitis b
41	74	100.0	130 2 Q8QPI1	Q8QPI1 hepatitis b
42	74	100.0	130 2 Q8QPI3	Q8QPI3 hepatitis b
43	74	100.0	130 2 Q8QPI4	Q8QPI4 hepatitis b
44	74	100.0	130 2 Q8QPI5	Q8QPI5 hepatitis b
45	74	100.0	130 2 Q8QPI6	Q8QPI6 hepatitis b

ALIGNMENTS

RESULT 1

ID	Q77BF4	PRELIMINARY;	PRT;	96 AA.
AC	Q77BF4;			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	Core antigen (Fragment).			
OS	Hepatitis B virus.			
OC	Virusess; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10407;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=genotype D; TISSUE=Blood;			
RX	MEDLINE=20381124; PubMed=10921962;			
RA	Petrosillo N., Ippolito G., Solfrosi L, Varaldo P.E., Clementi M.,			
RA	Manzin A.;			
RT	"Molecular epidemiology of an outbreak of fulminant hepatitis B.";			
RL	J. Clin. Microbiol. 38:2975-2981(2000).			
DR	EMBL; AJ010006; CAA08960.1; -			
DR	InterPro; IPR002006; Hepatitis_core.			
DR	Pfam; PF00906; Hepatitis_core; 1.			
DR	NON TER			
SQ	SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;			

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 41 TPPAYRPPNAPIL 53

RESULT 2

ID	Q77BF6	PRELIMINARY;	PRT;	96 AA.
AC	Q77BF6;			
DT	05-JUL-2004 (TREMBlrel. 27, Created)			
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)			
DE	Core antigen (Fragment).			
OS	Hepatitis B virus.			
OC	Virusess; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
OX	NCBI_TaxID=10407;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=genotype D; TISSUE=Blood;			
RX	MEDLINE=20381124; PubMed=10921962;			
RA	Petrosillo N., Ippolito G., Solfrosi L, Varaldo P.E., Clementi M.,			
RA	Manzin A.;			
RT	"Molecular epidemiology of an outbreak of fulminant hepatitis B.";			
RL	J. Clin. Microbiol. 38:2975-2981(2000).			
DR	EMBL; AJ010005; CAA08958.1; -			

DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11443 MW; FBA662E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPAYRPPNPAPIL 13
Db 41 TPAYRPPNPAPIL 53

RESULT 3

Q77BF8 PRELIMINARY; PRT; 96 AA.
AC Q77BF8.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Core antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype D; TISSUE=Blood;
RX MEDLINE=20381124; PubMed=10921962;
RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
Manzin A.;
RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
RL J. Clin. Microbiol. 38:2975-2981(2000).
DR EMBL; AJ010004; CA08956.1; -;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11443 MW; FBA662E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPAYRPPNPAPIL 13
Db 41 TPAYRPPNPAPIL 53

RESULT 4

Q77BG0 PRELIMINARY; PRT; 96 AA.
AC Q77BG0.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Core antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype D; TISSUE=Blood;
RX MEDLINE=20381124; PubMed=10921962;
RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
Manzin A.;
RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
RL J. Clin. Microbiol. 38:2975-2981(2000).
DR EMBL; AJ010003; CA08954.1; -;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11443 MW; FBA662E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPAYRPPNPAPIL 13
Db 41 TPAYRPPNPAPIL 53

RESULT 5

Q77BG1 PRELIMINARY; PRT; 96 AA.
AC Q77BG1.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Core antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype D; TISSUE=Blood;
RX MEDLINE=20381124; PubMed=10921962;
RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
Manzin A.;
RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
RL J. Clin. Microbiol. 38:2975-2981(2000).
DR EMBL; AJ010002; CA08952.1; -;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11443 MW; FBA662E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPAYRPPNPAPIL 13
Db 41 TPAYRPPNPAPIL 53

RESULT 6

Q77BG3 PRELIMINARY; PRT; 96 AA.
AC Q77BG3.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Core antigen (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=genotype D; TISSUE=Blood;
RX MEDLINE=20381124; PubMed=10921962;
RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
Manzin A.;
RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
RL J. Clin. Microbiol. 38:2975-2981(2000).
DR EMBL; AJ010000; CA08948.1; -;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON TER 1
SQ SEQUENCE 96 AA; 11443 MW; FBA662E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPAYRPPNPAPIL 13

Db 41 TPPAYRPPNAPIL 53

RESULT 7

077BG4 ID 077BG4 PRELIMINARY; PRT; 96 AA.
 AC 077BG4
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009999; CA08946.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

077BG5 ID 077BG5 PRELIMINARY; PRT; 96 AA.
 AC 077BG5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009998; CA08944.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9

077BH1 ID 077BH1 PRELIMINARY; PRT; 96 AA.
 AC 077BH1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009997; CA08942.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

077BG7 ID 077BG7 PRELIMINARY; PRT; 96 AA.
 AC 077BG7;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009997; CA08942.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

077BG9 ID 077BG9 PRELIMINARY; PRT; 96 AA.
 AC 077BG9;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009996; CA08940.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10

077BH1 ID 077BH1 PRELIMINARY; PRT; 96 AA.
 AC 077BH1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009996; CA08940.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

077BH1 ID 077BH1 PRELIMINARY; PRT; 96 AA.
 AC 077BH1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L., Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009996; CA08940.1;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER
 SO SEQUENCE 96 AA; 11443 MW; FBA62E745196B9E CRC64;
 Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009995; CA08938.1; -
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 1
 SQ SEQUENCE 96 AA; 11443 MW; FBA862E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 41 TPPAYRPPNAPIL 53

RESULT 12

ID Q77BH3 PRELIMINARY; PRT; 96 AA.
 AC Q77BH3;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ009994; CA08936.1; -
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 1
 SQ SEQUENCE 96 AA; 11443 MW; FBA862E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 41 TPPAYRPPNAPIL 53

RESULT 13

ID Q9YJM3 PRELIMINARY; PRT; 96 AA.
 AC Q9YJM3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RX MEDLINE=10407;
 FT NON TER 1

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=genotype D; TISSUE=Blood;
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ010007; CA08962.1; -
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 1
 SQ SEQUENCE 96 AA; 11443 MW; FBA862E745196B9E CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 41 TPPAYRPPNAPIL 53

RESULT 14

ID Q9YQ42 PRELIMINARY; PRT; 96 AA.
 AC Q9YQ42;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Core antigen (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RX MEDLINE=20381124; PubMed=10921962;
 RA Petrosillo N., Ippolito G., Solforosi L, Varaldo P.E., Clementi M.,
 Manzini A.;
 RT "Molecular epidemiology of an outbreak of fulminant hepatitis B.";
 RL J. Clin. Microbiol. 38:2975-2981(2000).
 DR EMBL; AJ010001; CA08950.1; -
 DR InterPro; IPR002006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 1
 SQ SEQUENCE 96 AA; 11428 MW; D46972F6440979BE CRC64;

Query Match 100.0%; Score 74; DB 2; Length 96;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
 DB 41 TPPAYRPPNAPIL 53

RESULT 15

ID Q80J61 PRELIMINARY; PRT; 113 AA.
 AC Q80J61;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Core protein.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 RX MEDLINE=15215682;
 FT NON TER 1
 SQ SEQUENCE FROM N.A.
 RX Luo K., Liu Z., He H., Peng J., Liang W., Dai W., Hou J.;
 RT "The putative recombination of hepatitis B virus genotype B with pre-

RT c/c region of genotype C."
 RL Virus Genes 29:31-41(2004).
 DR EMBL: AY217370; AAC63544.1; -
 DR InterPro: IPR002006; Hepatitis_core.
 DR Pfam: PF00906; Hepatitis_core; 2.
 SQ SEQUENCE 113 AA; 1306 MW; 3A0E460F2038C680 CRC64;

Query Match 100.0%; Score 74; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
 |||||
 Db 58 TTPAYRPPNAPIL 70

Search completed: December 14, 2004, 16:48:15
 Job time : 42.275 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:04 ; Search time 36.8875 Seconds
(without alignments)
126.424 Million cell updates/sec

Title: US-09-055-744A-10
Perfect score: 74
Sequence: 1 TTPAYRPPNAPIL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	74	100.0	13 2 AAR33501	AAR33501 T helper
2	74	100.0	13 2 AAR78929	AAR78929 HBC 128-1
3	74	100.0	13 2 AAW39439	AAW39439 Mouse H-2
4	74	100.0	13 2 AAW50117	AAW50117 Pan DR b1
5	74	100.0	13 3 AAY52556	AAY52556 HBV core
6	74	100.0	13 4 AAG64542	AAG64542 T-helper
7	74	100.0	13 4 AAE02681	AAE02681 Hepatitis
8	74	100.0	13 4 AAE00471	AAE00471 Hepatitis
9	74	100.0	13 4 AAG62426	AAG62426 Immunogen
10	74	100.0	13 4 AAB82775	AAB82775 Hepatitis
11	74	100.0	13 4 AAU00614	AAU00614 H-2 I-Ab-
12	74	100.0	13 5 AAU70851	AAU70851 Hepatitis
13	74	100.0	13 5 ABB76787	ABB76787 HBV pepti
14	74	100.0	13 5 ABG62860	ABG62860 Antigenic
15	74	100.0	13 5 ABP52344	ABP52344 TH epitop
16	74	100.0	13 5 ABP52307	ABP52307 T helper
17	74	100.0	13 5 ABP52350	ABP52350 TH epitop
18	74	100.0	13 5 ABP51503	ABP51503 T helper
19	74	100.0	13 6 ABR44095	ABR44095 HBV core
20	74	100.0	13 6 ABP98778	ABP98778 HBV core
21	74	100.0	13 6 AAO23990	AAO23990 p128-40 I
22	74	100.0	13 6 ABU65009	ABU65009 HBV core
23	74	100.0	13 7 ADC21494	ADC21494 Hepatitis
24	74	100.0	13 7 ADC85105	ADC85105 HBV assoc
25	74	100.0	13 7 ADD35647	ADD35647 Hepatitis

26	74	100.0	13 7 ADG38596	ADG38596 Hepatitis
27	74	100.0	13 7 ADI64650	ADI64650 HBV core
28	74	100.0	13 8 ADK14662	ADK14662 Hepatitis
29	74	100.0	13 8 ADM73996	ADM73996 Specific
30	74	100.0	13 8 ADN12176	ADN12176 Amino aci
31	74	100.0	14 3 AAY52571	AAY52571 HBV core
32	74	100.0	15 2 AAW01776	AAW01776 Hepatitis
33	74	100.0	15 2 AAY53554	AAY53554 HBV core
34	74	100.0	16 6 AAE33938	AAE33938 Hepatitis
35	74	100.0	18 6 AAR33958	AAR33958 Hepatitis
36	74	100.0	20 4 AAB67642	AAB67642 Peptide C
37	74	100.0	20 5 AAU70872	AAU70872 Hepatitis
38	74	100.0	20 7 ADC85126	ADC85126 Sequence
39	74	100.0	20 8 ADK14683	ADK14683 Hepatitis
40	74	100.0	21 1 AAP80955	AAP80955 T cell st
41	74	100.0	21 2 AAR82579	AAR82579 Hepatitis
42	74	100.0	21 2 AAW05605	AAW05605 Hepatitis
43	74	100.0	21 2 AAY13806	AAY13806 Hepatitis
44	74	100.0	21 3 AAY58772	AAY58772 Unidentifi
45	74	100.0	21 3 AAY80062	AAY80062 Pathogen

ALIGNMENTS

RESULT 1	AAAR33501
ID	AAAR33501 standard; peptide; 13 AA.
XX	
AC	AAAR33501;
DT	25-MAR-2003 (revised)
DT	01-JUL-1993 (first entry)
XX	
DE	T helper peptide HBC 128-140.
XX	
KW	Hepatitis B virus; HBV, core antigen; MHC class I; chronic; acute;
KW	infection; identification; HLA-restricted.
XX	
OS	Synthetic.
XX	
PN	WO9303764-A1.
XX	
PD	04-MAR-1993.
XX	
PF	26-AUG-1992; 92MO-US007218.
XX	
PR	26-AUG-1991; 91US-00749568.
PR	29-JAN-1992; 92US-00827682.
PR	27-APR-1992; 92US-00874491.
XX	
PA	(CYTE-) CYTEL CORP.
PI	Vitello MA, Chesnut RW;
XX	
DR	WPI; 1993-093728/11.
XX	
PT	Cytotoxic T-lymphocyte stimulating peptide(s) - derived from hepatitis B
PT	virus useful for treating, preventing and diagnosing infection.
XX	
PS	Disclosure; Page 21; 89pp; English.
XX	
CC	This is a T helper epitope peptide, the sequence of which is derived from
CC	hepatitis B virus (HBV) core antigen amino acids 128-140. It may be used
CC	in a conjugate with cytotoxic T-lymphocyte stimulating (CTL) peptides to
CC	enhance an individual's immunity by providing cell-mediated immunity and
CC	protective antibodies. (Updated on 25-MAR-2003 to correct PN field.)
XX	
SQ	Sequence 13 AA;
Query Match	100.0%; Score 74; DB 2; Length 13;
Best Local Similarity	100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 1 TPPAYRPPNAPIL 13
 |||||
 DB 1 TPPAYRPPNAPIL 13

RESULT 2

AAW8929 standard; peptide; 13 AA.

AAW8929;

25-MAR-2003 (revised)

27-MAR-1996 (first entry)

HBC 128-140 cytotoxic T lymphocyte epitope.

HBC 128-140; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte; antigens; treatment; disease prevention; hepatitis B.

Hepatitis B virus.

MO9522317-A1.

24-AUG-1995.

16-FEB-1995; 95WO-US002121.

16-FEB-1994; 94US-00197484.

(CYTE-) CYTEL CORP.

Vitello MA, Chesnut RW, Sette AD, Cells E, Grey H;

WPI; 1995-302545/39.

Compsn. inducing cytotoxic T lymphocyte response to pref. viral,

bacterial, parasitic or tumour antigens - useful in the treatment and

prevention of diseases associated with the antigen e.g. hepatitis B.

Example 4; Page 52; 109pp; English.

A compsn. which induces a cytotoxic T lymphocyte (CTL) response to a

hepatitis B virus (HBV) antigen (Ag) in a mammal comprises, a HBV CTL Ag

response inducing peptide (i.e. AAW8929) and a lipid conjugated helper T

cell inducing peptide. The compsn. is useful in the treatment and

prevention of hepatitis B. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TPPAYRPPNAPIL 13

1 TPPAYRPPNAPIL 13

AAW39439 standard; peptide; 13 AA.

AAW39439;

11-JUN-1998 (first entry)

Mouse H-2 I-Ab-restricted HBV core antigen-derived T helper epitope.

T cell epitope; immune response; human leukocyte antigen; HLA Class I;

vaccine; immunogenic; major histocompatibility complex; MHC; B cell;

disease; anti-tumour; anti-viral.

OS Synthetic.
 OS Mus sp.
 XX MO9741440-A1.
 XX 06-NOV-1997.

28-APR-1997; 97WO-NL000229.

26-APR-1996; 96EP-00201145.

23-DEC-1996; 96EP-00203670.

(UTLE-) RIJXSUNIV LEIDEN.

(SCIS-) SCI SEED CAPITAL INVESTMENTS BV.

Van Der Burg SH, Kast WM, Toes REM, Offringa R, Mellef CUM;

WPI; 1997-549891/50.

Method of selecting T cell peptide epitope(s) - by measuring the

stability of HLA class I-peptide complexes on intact B cells.

Example 2; Page 21; 109pp; English.

Peptides AAW39430-W39734 are used in a novel method for the selection of

immunogenic T-cell peptide epitopes present in polypeptide antigens.

Peptide AAW39439 is a mouse H-2 I-Ab restricted HBV core antigen-derived

T helper epitope which is injected into HLA-A*0201Kb transgenic mice. The

method involves the identification of peptide sequences capable of

binding to an HLA (human leukocyte antigen) class I molecule and

measuring the binding of this epitope peptide to the HLA class I peptide.

The stability of binding of the peptide and MHC (major histocompatibility

complex) class I molecule is measured on intact human B cells carrying

the MHC molecule at their cell surfaces. The method can be used to select

peptide epitopes for generating vaccines against a disease associated

with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are

especially T-cell peptide epitopes with strong anti-tumour and anti-viral

immune responses

Sequence 13 AA;

Query Match 100.0%; Score 74; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TPPAYRPPNAPIL 13

1 TPPAYRPPNAPIL 13

AAW50117 standard; peptide; 13 AA.

AAW50117;

30-JUN-1998 (first entry)

Pan DR binding peptide (14).

Pan DR binding peptide; antigen binding site; MHC molecule; DR locus.

Synthetic.

US5736142-A.

07-APR-1998.

14-SEP-1994; 94US-00305871.

14-SEP-1993; 93US-00121101.

(CYTE-) CYTEL CORP.

XX Sidney J, Sette A, Alexander JL, Gaeta F, Grey HM;
 PI WPI; 1998-239154/21.
 XX
 XX Peptides that bind to MHC molecules of all DR alleles - inhibiting or
 PT inducing MHC class II mediated activation of T cells.
 XX
 PS Example 5; Col 35-36; 29pp; English.
 XX
 CC The present sequence, a pan DR binding peptide, is capable of binding
 CC antigen binding sites on MHC molecules, which are encoded by most of the
 CC alleles of a DR locus. The peptide can be used to inhibit or induce MHC
 CC class II mediated activation of T-cells or helper T-cells, which
 CC themselves mediate a CTL response. The peptide can be used in mammals,
 CC especially humans, to inhibit T-cell-mediated events involved in
 CC allograft rejection, allergic responses and autoimmunity and as a vaccine
 CC adjuvant for enhancing an immune response against an administered
 CC immunogen. The peptide can be used with other immunogens to treat, e.g.
 CC prostate cancer, hepatitis B, hepatitis C, AIDS, renal and cervical
 CC carcinoma, lymphoma, CMV and condyloma acuminatum
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPIL 13
 1 TPPAYRPPNPIL 13
 Db
 RESULT 5
 AAY52556
 ID AAY52556 standard; peptide; 13 AA.
 XX
 AC AAY52556;
 XX
 DT 06-AUG-2003 (revised)
 DT 28-FEB-2000 (first entry)
 XX
 DE HBV core antigen MHC class II epitope, encoded by 180T fusion gene.
 XX
 XX Chimeric; pan DR epitope; expression vector; promoter;
 KM major histocompatibility complex; MHC; targeting; peptide; epitope;
 KM antigen; presentation; class I; cytosolic pathway; endoplasmic reticulum;
 KM class II; extracellular antigen; endocytic pathway; helper T lymphocyte;
 KM HTL; universal epitope; cytotoxic T lymphocyte; CTL; immune response;
 KM immunogenicity; assay; vaccine; immunity; infection; pathogen; virus;
 KM HIV; HBV; HCV; hepatitis B; hepatitis C; bacterium; protozoan;
 KM tumour cell; autoimmune disease; activation; antiviral; antimarialar;
 KM immunoprotective; core antigen.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN WO958658-A2.
 PD 18-NOV-1999.
 XX
 PF 13-MAY-1999; 99WO-US010646.
 XX
 PR 13-MAY-1998; 98US-00078904.
 PR 15-MAY-1998; 98US-0085751P.
 XX
 PA (EPIM-) EPIMMUNE INC.
 PI Fikes JD, Hermanson GG, Sette A, Ishioka GY, Livingston B;
 PI Chesnut RW;
 DR WPI; 2000-039103/03.
 XX

PT Expression vectors encoding major histocompatibility targeting sequence,
 PT used as, e.g. tumor vaccines.
 XX
 XX
 PS Example 1; Page 36; 130pp; English.
 XX
 CC This sequence represents a hepatitis B virus (HBV) core antigen MHC class
 CC II epitope, encoded by the 180T fusion gene (AA238617), used in an
 CC exemplification of the present invention. The invention relates to a
 CC novel expression vector comprising a promoter operably linked to a fusion
 CC gene encoding a major histocompatibility complex (MHC) targeting
 CC sequence, and two or more heterologous peptide epitopes. The MHC
 CC targeting sequence may be a class I targeting sequence, which directs
 CC an MHC class I epitope to a cytosolic pathway or to the endoplasmic
 CC reticulum, or an MHC class II targeting sequence, which directs
 CC extracellular antigens to enter the endocytic pathway to be processed
 CC into antigen peptides for presentation on MHC class II molecules. The
 CC heterologous epitopes may comprise either helper T lymphocyte (HTL)
 CC epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
 CC epitope such as a pan DR epitope (PADRE). The vectors are useful for
 CC stimulating an immune response in vivo, as well as for use in assaying
 CC the human immunogenicity of a human T cell peptide epitope in vivo in a
 CC non-human mammal. They provide a nucleic acid vaccine for enhancing
 CC immunity against infectious pathogens, such as viruses (e.g., HIV,
 CC hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,
 CC Plasmodium falciparum, the cause of malaria) and also tumour cells and
 CC autoimmune diseases. Universal MHC class II epitopes are advantageously
 CC combined with other MHC class I and class II epitopes to increase the
 CC number of cells that are activated in response to a given antigen and
 CC provide a broader population coverage of MHC-reactive alleles. (Updated
 CC on 06-AUG-2003 to correct OS field.)
 CC
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNPIL 13
 1 TPPAYRPPNPIL 13
 Db
 RESULT 6
 AAG64542
 ID AAG64542 standard; peptide; 13 AA.
 XX
 AC AAG64542;
 XX
 DT 22-OCT-2001 (first entry)
 DT 22-OCT-2001 (first entry)
 XX
 DE T-helper epitope peptide.
 XX
 KM Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
 KM human immunodeficiency virus; vaccine; T-helper.
 XX
 OS Synthetic.
 OS
 PN WO200155177-A2.
 PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-DK000059.
 XX
 PR 28-JAN-2000; 2000EP-00610017.
 PR 31-JAN-2000; 2000US-0179333P.
 XX
 PA (STAT-) STATENS SERUM INST.
 PI Fomsgaard A, Brunak S, Buus S, Corbet S, Laemmoller SL, Hansen J;
 PI WPI; 2001-476184/51.
 DR
 XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-

PT HIV vaccines.
 XX
 PS Example 7; Page 42; 383pp; English.
 XX
 CC The invention relates to identification of cytotoxic T cell lymphocyte
 CC (CTL) epitopes (AAW22116-AAW23484) that generate anti-HIV activity. CTL
 CC are a major protective mechanism against viral diseases. Antibodies may
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
 CC prevent infection of cells in the host, but CTL will limit viral
 CC production by killing the cell. The CTL epitopes are useful in medicine,
 CC in the manufacture of vaccines or diagnostic agents. The present sequence
 CC is that of a T-helper epitope peptide useful to the invention
 CC
 XX Sequence 13 AA;
 SQ
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13
 RESULT 7
 AAE02681
 ID AAE02681 standard; peptide; 13 AA.
 XX
 AC AAE02681;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Hepatitis B virus HBVc helper peptide.
 XX
 KW Cytostatic; antibacterial; antifungal; gene therapy; vaccine; antiviral;
 KW tumour; epitope; glycoprotein; hepatitis B virus; HBV; immune response;
 KW CTL; cytotoxic T lymphocyte; HLA; human leucocyte antigen.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200127291-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-EP009902.
 XX
 PR 12-OCT-1999; 99US-0158356P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Firat H, Lemonnier F, Langlade-Demoyen P;
 DR WPI; 2001-282038/29.
 XX
 PT New polynucleotide comprising at least one viral, fungal, bacterial, or
 PT tumour epitope of an antigen, capable of inducing a cellular response.
 XX
 PS Example 1; Page 23; 70pp; English.
 XX
 CC The invention relates to polynucleotide containing at least a part of the
 CC coding sequence of the middle glycoprotein of hepatitis B virus (HBV) in
 CC which is inserted a DNA sequence coding for an epitope comprising at
 CC least one viral, fungal, bacterial, or tumour epitope of an antigen,
 CC capable of inducing a cellular response. Nucleic acids and compositions
 CC of the invention are useful for inducing in vivo a CTL (cytotoxic T
 CC lymphocyte) response against several epitopes of one or more, bacterial,
 CC viral, fungal, or tumour antigens. A composition of the invention
 CC produces an immune response against HIV antigen and are used in the
 CC production of vaccines. The polynucleotides of the invention are also
 CC used in gene therapy. The present sequence is hepatitis B virus helper
 CC peptide. This peptide is co-injected with human epitopes in order to
 CC elicit HLA (human leucocyte antigen) -A2.1-restricted CTL response in
 CC mice

XX Sequence 13 AA;
 SQ
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13
 RESULT 8
 AAE00471
 ID AAE00471 standard; peptide; 13 AA.
 XX
 AC AAE00471;
 XX
 DT 19-JUN-2001 (first entry)
 XX
 DE Hepatitis B virus core (HBVc) tumour epitopic peptide.
 XX
 KW Tumour epitope; cytostatic; immunostimulant; gene therapy;
 KW middle glycoprotein; Hepatitis B virus core; cytotoxic response;
 KW immune response; cytotoxic T lymphocyte; CTL; HBVc; HLA;
 KW human leucocyte antigen.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200123577-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 29-SEP-2000; 2000WO-EP009900.
 XX
 PR 30-SEP-1999; 99US-0156945P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Firat H, Lemonnier F, Langlade-Demoyen P, Michel M, Subrbler AA;
 DR WPI; 2001-266164/27.
 XX
 PT Novel polynucleotide having DNA sequence encoding tumor antigen epitope
 PT inserted in part of coding sequence of middle glycoprotein of hepatitis B
 PT virus, used to induce immune response against tumor-specific antigen.
 XX
 PS Example 1; Page 13; 36pp; English.
 XX
 CC The present invention relates to an isolated or purified polynucleotide
 CC containing a DNA sequence coding for at least one tumour epitope of a
 CC tumour antigen inserted into part of the coding sequence of the middle
 CC glycoprotein of the Hepatitis B virus (HBV). The polynucleotide is useful
 CC for optionally evaluating cytotoxic responses in the individual's
 CC lymphocyte population. It induces an immune response against at least one
 CC tumour specific antigen or tissue specific antigen. The vector comprising
 CC the polynucleotide induces in vivo, cellular and/or humoral immune
 CC response. The composition comprising the polynucleotide induces in vivo,
 CC cytotoxic T lymphocyte (CTL) against one or more antigens or epitopes
 CC present on the hybrid protein. The polynucleotide is also useful in gene
 CC therapy. The present sequence is a Hepatitis B virus core (HBVc) tumour
 CC epitopic peptide. This peptide elicits HLA (human leucocyte antigen)-A2.1
 CC - restricted CTL response in mice
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPAYRPPNAPIL 13
 DB 1 TPPAYRPPNAPIL 13

RESULT 9
 AAG62426 standard; peptide; 13 AA.
 AC AAG62426;
 DT 03-SEP-2001 (first entry)
 DE Immunogenic peptide HBV core SEQ ID 30.
 DE Class I epitope; immunogenic; heteroclitic analogue; immune response;
 KM antigen display; viral disease; cancer.
 OS Synthetic.
 PN WO200136452-A2.
 PD 25-MAY-2001.
 PD 20-NOV-2000; 2000WO-US031856.
 PR 18-NOV-1999; 99US-0166529P.
 PR 06-OCT-2000; 2000US-0239008P.
 XX (EPIM-) EPIMUNE INC.
 PI Tangri S, Sette A, Ishioka G;
 DR WPI; 2001-355609/37.
 XX
 PT Enhancing immunogenicity of peptide containing class I epitope, useful
 PT for treating cancer, comprises providing (seeml-)conservative amino acid
 PT substitutions at specified positions of these epitopes.
 PS Disclosure; Fig 1A; 96pp; English.
 XX
 CC This invention relates to a method of enhancing the immunogenicity of a
 CC peptide, where the peptide contains a class I epitope. The invention
 CC includes methods for preparing peptides containing epitopes which have
 CC enhanced ability to effect an immune response (compared to wild-type
 CC epitopes). The peptides are referred to as heteroclitic analogues. The
 CC method is useful for eliciting an immune response by contacting CTLs with
 CC the immunogenically enhanced peptide in vitro in the presence of an
 CC antigen presenting cell, or by administering to a subject a nucleic acid
 CC molecule comprising a nucleotide sequence encoding the peptide. The
 CC peptides are useful as reagents to evaluate an immune response and the
 CC efficacy of the vaccine, and for making antibodies. The heteroclitic
 CC analogues are useful in immunological compositions for the treatment of
 CC viral diseases, cancer, and other conditions which are characterised by
 CC displayed antigens on target cells. The present sequence represents a
 CC class I epitope which may be used in the method of the invention
 CC
 SQ Sequence 13 AA;
 QY Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 TTPAYRPPNAPIL 13
 1 TTPAYRPPNAPIL 13
 1 TTPAYRPPNAPIL 13
 RESULT 10
 AAB82775 standard; protein; 13 AA.
 AC AAB82775;
 DT 06-AUG-2003 (revised)
 DT 29-OCT-2001 (first entry)

XX Hepatitis B core antigen peptide.
 XX
 KM Telomerase reverse transcriptase; hTERT; human; cytotoxic T lymphocyte;
 KM major histocompatibility complex; cancer; tumour;
 KM human leucocyte antigen; HLA-A2.1; HBV; vaccine.
 OS Hepatitis B virus.
 PN WO200160391-A1.
 PD 23-AUG-2001.
 PD 15-FEB-2001; 2001WO-US005143.
 PR 15-FEB-2000; 2000US-0182685P.
 PR 15-FEB-2001; 2001US-00182685.
 PA (REGC) UNIV CALIFORNIA.
 PI Zanetti M;
 DR WPI; 2001-536552/59.
 XX
 PT Vaccine for initiating and enhancing a cytotoxic T lymphocyte response,
 PT for treating cancers or tumors or for inducing immune response against
 PT tumors, comprises a telomerase reverse transcriptase peptide.
 PS Example 1; Page 12; 52pp; English.
 XX
 CC The present sequence is that of a hepatitis B virus core antigen (HBVc)
 CC peptide comprising amino acid residues 128-140. The peptide was used to
 CC immunise HMD mice and results were compared with those obtained using
 CC human telomerase reverse transcriptase (hTERT) HLA-A2.1+ restricted
 CC peptide p540 (see AAB82772). The induction of CTL responses in vitro and
 CC in vivo, and the susceptibility to lysis of tumour cells of various
 CC origins by hTERT CTL suggest that hTERT could serve as a universal cancer
 CC vaccine for humans. A claimed universal vaccine for treating tumours of
 CC any origin comprises at least 1 hTERT peptide. The peptide is 7-15 amino
 CC acid residues in length and may be modified to enhance binding to the
 CC major histocompatibility complex. Also claimed is a method for inducing
 CC and enhancing a CTL response against cancer cells, involving harvesting
 CC blood leucocytes, pulsing with hTERT, and contacting cancer cells with the
 CC pulsed leucocytes. A method for targeting CTL to tumour cells is also
 CC claimed, and involves administering a hTERT peptide to a mammal,
 CC especially a cancer patient. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 SQ Sequence 13 AA;
 QY Query Match 100.0%; Score 74; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 TTPAYRPPNAPIL 13
 1 TTPAYRPPNAPIL 13
 1 TTPAYRPPNAPIL 13
 RESULT 11
 AAU00614 standard; peptide; 13 AA.
 AC AAU00614;
 DT 12-SEP-2001 (first entry)
 DE H-2 i-Ab-restricted HBV core antigen-derived T helper epitope.
 DE Human; MHC1; antigenic peptide; major histocompatibility complex; MHC-I;
 KM glycoprotein; cytotoxic T lymphocytes; T cell response; cancer; vaccine;
 KM cancer gene therapy; diagnosis; treatment; inflammatory disorder; HBV;
 KM organ transplant rejection; graft versus host disease.

```

XX OS Hepatitis B virus.
XX PN WO200118035-A2.
XX PD 15-MAR-2001.
XX PF 07-SEP-2000; 2000WO-EP008761.
XX PR 08-SEP-1999; 99GB-00021242.
XX PR 10-SEP-1999; 99EP-00402237.
XX PR 03-MAR-2000; 2000US-0187215P.
XX PA (TRGE ) TRANSGENE SA.
XX PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
XX PI Taylor-Papadimitriou J, Heukamp LC, Offringa R, Melief CJM,
XX PI Acres B, Thomas M;
XX DR WPI; 2001-235187/24.
XX PS
XX PT New antigenic polypeptides of MUC-1 protein which activate cytotoxic T
XX PT lymphocyte proteins and their analogs, useful for identifying a major
XX PT histocompatibility complex class I restricted T cell response and for
XX PT diagnosing cancer.
XX PS Example 5; Page 42; 81pp; English.
XX CC The sequence represents an H-2 I-Ab-restricted hepatitis B virus (HBV)
XX CC core antigen-derived T helper epitope used in testing of human MUC1
XX CC polypeptide derivatives through a cytotoxic T lymphocyte (CTL) assay.
XX CC Derivative antigenic peptides of MUC1 protein bind at least one major
XX CC histocompatibility complex class I (MHC-I) glycoprotein, which activates
XX CC cytotoxic T lymphocytes to induce a protective response against tumours.
XX CC Diagnosis of cancer involves determining the presence or absence in a
XX CC host cell of MHC class I restricted T cell response to a MUC1 derivative,
XX CC where the presence of the MHC class I restricted T cell response
XX CC indicates that the host has cancer. Measurement of the level of MHC class
XX CC I restricted T cell response is also useful to monitor the severity of
XX CC cancer, a larger response indicating a more severe cancer. MUC1
XX CC derivatives are useful in cancer therapy and to follow MUC1 specific
XX CC immune responses in patients during the course of disease and/or
XX CC treatment. MUC1 DNA is useful in cancer gene therapy, vaccination and
XX CC diagnosis. Compositions of the sequences are used in vaccines and
XX CC treatments against cancer or diseases caused by an immune response, such
XX CC as an inflammatory disorder, organ transplant rejection or graft versus
XX CC host disease
XX SQ Sequence 13 AA;
XX
XX Query Match 100.0%; Score 74; DB 4; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.0014;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTPAYRPPNAPIL 13
XX |||||||||
DB 1 TTPAYRPPNAPIL 13

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XX OS Synthetic.
XX PN WO200181421-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-IB000844.
XX PR 21-APR-2000; 2000US-00556605.
XX PA (TRIIP-) TRIPEP AB.
XX PI Sallberg M;
XX DR WPI; 2002-055347/07.
XX PT Novel peptide that binds to hepatitis B virus core or E antigen, useful
XX PT for creating and preventing hepatitis B virus infection.
XX PS Example 6; Page 28; 82pp; English.
XX CC The invention relates to an isolated or purified peptide (I) which binds
XX CC Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen (HBeAg).
XX CC (I) is useful for creating or preventing Hepatitis B virus (HBV)
XX CC infection, by identifying a subject in need of a molecule that inhibits
XX CC HBV infection, and providing the subject with (I). (I) is also useful for
XX CC determining the presence of HBV in a biological sample, and for
XX CC inhibiting B cell mediated processing and uptake of HBcAg and/or HBeAg,
XX CC by determining whether (I) inhibits B cell mediated processing and uptake
XX CC of HBcAg and/or HBeAg by performing an assay of T cell proliferation or
XX CC cytokine production. (I) is also useful for modulating an immune system
XX CC response. (I) is useful as a template for a design of synthetic molecules
XX CC including peptides, derivatives or modified peptides, peptidomimetics and
XX CC chemicals. (I) is also useful as biotechnological tool, diagnostic
XX CC reagent and as active ingredient in pharmaceuticals. (I) is also useful
XX CC as detection reagents in conventional immunohistochemical techniques, as
XX CC diagnostic reagents to detect HBV in biological sample, and to determine
XX CC the efficacy of an HBV treatment protocol by monitoring the levels of
XX CC HBeAg and/or HBcAg during and after treatment. AAU70766-AAU70876
XX CC represent Hepatitis B virus (HBV) core antigen (HBcAg) or HBV E antigen
XX CC (HBeAg) binding partners as described in the invention
XX SQ Sequence 13 AA;
XX
XX Query Match 100.0%; Score 74; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.0014;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TTPAYRPPNAPIL 13
XX |||||||||
DB 1 TTPAYRPPNAPIL 13

```

```

RESULT 12
AAU70851
ID AAU70851 standard; peptide; 13 AA.
XX
XX AC AAU70851;
XX
XX DT 14-FEB-2002 (first entry)
XX
XX DE Hepatitis B virus antigen binding partner #83.
XX
XX KM Hepatitis B virus; virocidic; immunomodulator; hepatotropic; HBV;
XX KM antiinflammatory; HBV core antigen; HBcAg; HBV E antigen; HBeAg;
XX KM B cell mediated processing; T cell proliferation; cytokine production;
XX KM immune system response.

```

```

RESULT 13
ABB76787
ID ABB76787 standard; peptide; 13 AA.
XX
XX AC ABB76787;
XX
XX DT 31-MAY-2002 (first entry)
XX
XX DE HBV peptide 128-140.
XX
XX KM Antiviral; anti-HIV; cytostatic; epitope; HLA A2.1;
XX KM human leukocyte antigen; immunotherapy; cancer; viral infection; vaccine.
XX
XX OS Unidentified.
XX
XX PN FR2812087-A1.
XX
XX PD 25-JAN-2002.
XX

```

PF 21-JUL-2000; 2000FR-00009591.
 XX
 PR 21-JUL-2000; 2000FR-00009591.
 XX
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Kometopoulos K, Tourdot S, Scardino A, Gross DA;
 XX WPI; 2002-189846/25.
 DR
 XX
 PT Identifying subdominant or cryptic epitopes, useful in immunotherapy of
 PT cancer and viral infection, comprises testing modified, non-immunogenic
 PT peptides for induction of cytotoxic T cells.
 CC
 XX
 PS Example 1; Page 14; 62pp; French.
 CC The present invention relates to subdominant/cryptic epitopes that are
 CC presented by HLA (human leukocyte antigen) Class I molecule A2.1. The
 CC epitopes or chimeric polypeptides containing them and nucleic acid
 CC encoding them are useful for preventative or curative immunotherapy of
 CC cancer and viral infections, particularly where used as vaccines. The
 CC present peptide was used to illustrate the invention
 CC
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPIYRPPNPAPIL 13
 DB 1 TPPIYRPPNPAPIL 13
 RESULT 14
 ID ABG62860 standard; peptide; 13 AA.
 XX
 AC ABG62860;
 XX
 DT 21-AUG-2002 (first entry)
 XX
 DE Antigenic domain peptide from a Hepatitis B virus protein.
 KM Ligand/receptor specificity exchanger; antibody; pathogen receptor;
 KM bacterial infection; viral infection; yeast infection; cancer;
 KM parasitic infection; fungal infection; proliferation; antibacterial;
 KM virucide; cytostatic; antifungal; antigenic domain.
 XX
 OS Hepatitis B virus.
 XX
 PN WO200224887-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 19-SEP-2001; 2001WO-IB002327.
 XX
 PR 19-SEP-2000; 2000US-00664025.
 XX
 PA (TRIP-) TRIPAP AB.
 XX
 PI Sallberg M, Flock J;
 DR WPI; 2002-489707/52.
 XX
 PT Novel ligand/receptor specificity exchanger that redirects antibodies to
 PT receptors on pathogen or tumor cell, has specificity domain having ligand
 PT for receptor, and antigenic domain having epitope of pathogen or toxin.
 CC
 XX Claim 14; Page 14; 79pp; English.
 PS The present invention relates to ligand/receptor specificity exchangers
 CC comprising at least one specificity domain comprising a ligand for a

CC receptor, and at least one antigenic domain joined to the specificity
 CC domain, where the ligand/receptor specificity exchangers redirect antibodies to
 CC toxin. The ligand/receptor specificity exchangers redirect antibodies to
 CC receptors present on pathogens. They are useful for preventing and
 CC treating human diseases such as bacterial, viral, yeast, parasitic and
 CC fungal infections, and cancer. These compositions act by inhibiting
 CC proliferation of pathogens, or cancer cells. One of the prophylactic
 CC applications of the ligand/receptor specificity exchangers includes
 CC coating or crosslinking it to a medical device or implant which include
 CC implantable medical devices that tend to serve as foci for infection by a
 CC number of bacterial species. ABG62853-ABG62869 represent antigenic domain
 CC peptides used in the methods of the present invention
 CC
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPPIYRPPNPAPIL 13
 DB 1 TPPIYRPPNPAPIL 13
 RESULT 15
 ID ABP52344 standard; peptide; 13 AA.
 XX
 AC ABP52344;
 XX
 DT 17-OCT-2002 (first entry)
 XX
 DE TH epitope.
 XX
 KM Cytotoxic T lymphocyte; CTL; T helper; MAGE3; cytotoxic T cell response;
 KM tumour; immune response; cancer; vaccine; antibody.
 XX
 OS Synthetic.
 XX
 PN WO200258728-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 28-JAN-2002; 2002WO-GB000354.
 XX
 PR 26-JAN-2001; 2001GB-00002145.
 XX
 PA (SCAN-) SCANCEL LTD.
 PA (SCAN-) CANCER RES CAMPAIGN TECHNOLOGY.
 XX
 PI Durrant LG, Parsons T, Robins A;
 XX
 DR WPI; 2002-608418/65.
 XX
 PT Use of polypeptides and nucleic acids encoding the polypeptides, in
 PT manufacturing medicament for stimulating a cytotoxic T cell response and
 PT for preventing or treating cancer, e.g. colorectal, lung, breast or
 PT ovarian cancer.
 CC
 XX Example 11; Page 45; 87pp; English.
 PS The present invention describes the use of a polypeptide (I) in the
 CC manufacture of a medicament for stimulating a cytotoxic T cell response,
 CC where (I) comprises a first portion comprising the part of human Fc that
 CC binds to CD64 and a second portion comprising one or more heterologous T
 CC cell epitopes. Also described is a method of stimulating a cytotoxic T
 CC cell response in a patient such as a mammal, preferably human, by
 CC administering (I) to the patient. (I) has cytostatic activity and can be
 CC used in vaccine production. (I) and the nucleic acid encoding (I) are
 CC useful in the manufacture of a medicament for stimulating cytotoxic T
 CC cell response. The medicament is useful for preventing and/or treating
 CC cancer, e.g. colorectal, lung, breast, gastric or ovarian cancer. The
 CC medicament stimulates cytotoxic and helper T cell responses. The

CC antibodies are useful as vaccines to stimulate helper and cytotoxic T
 CC cell responses. The polypeptides and nucleic acids are useful in
 CC optimising immunisation schedules for enhancing a protective immune
 CC response against cancer. The present sequence represents a TH epitope
 CC which is used in an example from the present invention
 XX

XX Sequence 13 AA;

Query Match 100.0%; Score 74; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
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 Db 1 TPPAYRPPNAPIL 13

Search completed: December 14, 2004, 16:42:02
 Job time : 38.8875 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 14, 2004, 16:38:07 ; Search time 8.775 Seconds
(without alignments)
98.249 Million cell updates/sec

Title: US-09-055-744A-10
Perfect score: 74
Sequence: 1 TPPAYRPPNAPIL 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	13	1 US-08-305-871A-14	Sequence 14, Appl
2	74	100.0	13	3 US-08-464-496-19	Sequence 19, Appl
3	74	100.0	13	4 US-08-788-822A-16	Sequence 16, Appl
4	74	100.0	13	4 US-08-197-484-113	Sequence 113, App
5	74	100.0	13	4 US-09-311-784A-49	Sequence 49, Appl
6	74	100.0	13	4 US-09-664-945-50	Sequence 50, Appl
7	74	100.0	13	5 PCT-US92-07218-19	Sequence 19, Appl
8	74	100.0	13	5 PCT-US95-02121-113	Sequence 113, App
9	74	100.0	14	4 US-09-311-784A-124	Sequence 124, App
10	74	100.0	15	3 US-08-737-886-7	Sequence 7, Appl
11	74	100.0	15	5 PCT-US96-09951-7	Sequence 7, Appl
12	74	100.0	21	3 US-09-100-409A-45	Sequence 45, Appl
13	74	100.0	21	5 PCT-US95-13841-13	Sequence 13, Appl
14	74	100.0	23	4 US-08-464-496-20	Sequence 20, Appl
15	74	100.0	23	4 US-08-197-484-114	Sequence 114, App
16	74	100.0	23	5 PCT-US92-07218-20	Sequence 20, Appl
17	74	100.0	23	5 PCT-US95-02121-114	Sequence 114, App
18	74	100.0	26	3 US-08-464-496-21	Sequence 21, Appl
19	74	100.0	26	4 US-08-197-484-115	Sequence 115, App
20	74	100.0	26	5 PCT-US92-07218-21	Sequence 21, Appl
21	74	100.0	26	5 PCT-US95-02121-115	Sequence 115, App
22	74	100.0	80	4 US-09-311-784A-8	Sequence 8, Appl
23	74	100.0	80	4 US-09-311-784A-10	Sequence 10, Appl
24	74	100.0	118	4 US-09-311-784A-12	Sequence 12, Appl
25	74	100.0	136	4 US-09-311-784A-4	Sequence 4, Appl
26	74	100.0	138	4 US-09-311-784A-4	Sequence 4, Appl
27	74	100.0	138	4 US-09-311-784A-4	Sequence 4, Appl

28	74	100.0	152	4 US-09-311-784A-20	Sequence 20, Appl
29	74	100.0	154	3 US-08-968-747-1	Sequence 1, Appl
30	74	100.0	155	3 US-08-968-747-17	Sequence 17, Appl
31	74	100.0	159	3 US-08-445-585-3	Sequence 3, Appl
32	74	100.0	161	3 US-08-968-747-19	Sequence 19, Appl
33	74	100.0	164	4 US-09-311-784A-18	Sequence 18, Appl
34	74	100.0	183	3 US-08-968-747-20	Sequence 20, Appl
35	74	100.0	183	3 US-09-248-588-2	Sequence 2, Appl
36	74	100.0	183	3 US-09-248-588-4	Sequence 4, Appl
37	74	100.0	183	5 PCT-US96-10602-12	Sequence 12, Appl
38	74	100.0	185	1 US-07-739-642-2	Sequence 2, Appl
39	74	100.0	185	1 US-07-739-642-4	Sequence 4, Appl
40	74	100.0	185	1 US-07-739-642-8	Sequence 8, Appl
41	74	100.0	185	1 US-07-739-642-10	Sequence 10, Appl
42	74	100.0	185	1 US-07-739-643-2	Sequence 2, Appl
43	74	100.0	185	1 US-07-739-643-4	Sequence 4, Appl
44	74	100.0	185	1 US-07-739-643-8	Sequence 8, Appl
45	74	100.0	185	1 US-07-739-643-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-305-871A-14
; Sequence 14, Application US/08305871A
; Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffrey L.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,871A
FILING DATE: 14-SEP-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,101
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-0062-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-305-871A-14
Query Match 100.0%; Score 74; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPAYRPPNAPIL 13
| | | | | | | | | |
Db 1 TTPAYRPPNAPIL 13

RESULT 2
US-08-464-496-19
Sequence 19, Application US/08464496
Patent No. 6122789
GENERAL INFORMATION:
APPLICANT: Epiimmune, Inc.
APPLICANT: Vitiello, Maria
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPITOPES
FILE REFERENCE: 39963-20001.13
CURRENT APPLICATION NUMBER: US/08/464,496
CURRENT FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 07/935,811
PRIOR FILING DATE: 1992-08-26
PRIOR APPLICATION NUMBER: 07/874,491
PRIOR FILING DATE: 1992-04-27
PRIOR APPLICATION NUMBER: 07/827,682
PRIOR FILING DATE: 1992-01-29
PRIOR APPLICATION NUMBER: 07/749,568
PRIOR FILING DATE: 1991-08-26
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-19

Query Match 100.0%; Score 74; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPAYRPPNAPIL 13
| | | | | | | | | |
Db 1 TTPAYRPPNAPIL 13

RESULT 3
US-08-788-822A-16
Sequence 16, Application US/08788822A
Patent No. 6413935
GENERAL INFORMATION:
APPLICANT: Alexander, Jeffrey L.
APPLICANT: Defrees, Shawn
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Induction of Immune Response Against
TITLE OF INVENTION: Desired Determinants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,822A
FILING DATE: 23-JAN-1997

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,510
FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-0092100S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-788-822A-16

Query Match 100.0%; Score 74; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTPAYRPPNAPIL 13
| | | | | | | | | |
Db 1 TTPAYRPPNAPIL 13

RESULT 4
US-08-197-484-113
Sequence 113, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esben
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-113

Query Match
Best Local Similarity 100.0%; Score 74; DB 4; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 5
US-09-311-784A-49
Sequence 49, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-09-311-784A-49

Query Match
Best Local Similarity 100.0%; Score 74; DB 4; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 6
US-09-664-945-50
Sequence 50, Application US/09664945
Patent No. 6660842
GENERAL INFORMATION:
APPLICANT: Matti Salberg
TITLE OF INVENTION: LIGAND/RECEPTOR SPECIFICITY EXCHANGERS
FILE REFERENCE: TRIPER.007C3
CURRENT APPLICATION NUMBER: US/09/664,945
CURRENT FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/532,106
PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 09/246,258
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 08/737,085
PRIOR FILING DATE: 1996-12-27
PRIOR APPLICATION NUMBER: SE 9401460
PRIOR FILING DATE: 1994-04-28
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antigenic domain peptide
US-09-664-945-50

Query Match
Best Local Similarity 100.0%; Score 74; DB 4; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
Db 1 TTPAYRPPNAPIL 13

RESULT 7
PCT-US92-07218-19
Sequence 19, Application PC/TUS9207218
GENERAL INFORMATION:
APPLICANT: Vitello, Maria A.
APPLICANT: Chesnut, Robert W.
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPITOPES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/07218
FILING DATE: 19920826
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14137-26-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US92-07218-19

Query Match 100.0%; Score 74; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
|||
Db 1 TTPAYRPPNAPIL 13

RESULT 8

PCT-US95-02121-113

; Sequence 113, Application PC/TUS9502121

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING

; TITLE OF INVENTION: CTL IMMUNITY

; NUMBER OF SEQUENCES: 153

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/02121

; FILING DATE: 16-FEB-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/197,484

; FILING DATE: 16-FEB-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/874,491

; FILING DATE: 27-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/827,682

; FILING DATE: 29-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/749,568

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 14137-26-4PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 467-9600

; TELEFAX: (415) 543-5043

; INFORMATION FOR SEQ ID NO: 113:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; PCT-US95-02121-113

Query Match 100.0%; Score 74; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
|||
Db 1 TTPAYRPPNAPIL 13

RESULT 9

PCT-US95-16415-9

; Sequence 9, Application PC/TUS9516415

; GENERAL INFORMATION:

; APPLICANT: The Scripps Research Institute

; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC

; TITLE OF INVENTION: CYTOTOXIC T CELLS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: The Scripps Research Institute

; STREET: 10666 North Torrey Pines Road, TPC-8

; CITY: La Jolla

; STATE: California

; COUNTRY: US

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/16415

; FILING DATE: 13-DEC-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/355,558

; FILING DATE: 14-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Logan, April C.

; REGISTRATION NUMBER: 33,950

; REFERENCE/DOCKET NUMBER: 433.1PC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 554-2937

; TELEFAX: (619) 554-6312

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; PCT-US95-16415-9

Query Match 100.0%; Score 74; DB 5; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTPAYRPPNAPIL 13
|||
Db 1 TTPAYRPPNAPIL 13

RESULT 10

US-09-311-784A-124

; Sequence 124, Application US/09311784A

; Patent No. 6534482

; GENERAL INFORMATION:

; APPLICANT: Fikes, John D.

; APPLICANT: Fikes, Gary G.

; APPLICANT: Sette, Alessandro

; APPLICANT: Ishioka, Glenn Y.

; APPLICANT: Livingston, Brian

; APPLICANT: Chesnut, Robert W.

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Expression Vectors for Stimulating an

; TITLE OF INVENTION: Immune Response and Methods of Using the Same

; FILE REFERENCE: 39963-20022.01

; CURRENT FILING DATE: US/09/311,784A

; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: US 60/085,751

; NUMBER OF SEQ ID NOS: 463

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 124

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HBVcore128

US-09-311-784A-124

Query Match 100.0%; Score 74; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
13
1 TTPAYRPPNAPIL 13
Db

RESULT 11
US-08-737-896-7

; Sequence 7, Application US/08737896
; Patent No. 6168804
; GENERAL INFORMATION:
; APPLICANT: Samuel, John
; APPLICANT: Kwon, Glen S.
; TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC
; TITLE OF INVENTION: IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: PACESEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737, 896
; FILING DATE: 24-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480, 499
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09551
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07254/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5039
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Hbcag
; US-08-737-896-7

Query Match 100.0%; Score 74; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
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1 TTPAYRPPNAPIL 13
Db

RESULT 12
PCT-US96-09951-7
; Sequence 7, Application PC/TUS9609951
; GENERAL INFORMATION:
; APPLICANT: The Governors of the University of Alberta
; TITLE OF INVENTION: A METHOD FOR ELICITING A TH1-SPECIFIC

; TITLE OF INVENTION: IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/09951

FILING DATE: 06-JUN-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Learn, June M.

REGISTRATION NUMBER: 31,238

REFERENCE/DOCKET NUMBER: 07254/037001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 678-5070

TELEFAX: (619) 678-5099

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: Hbcag

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..15

PCT-US96-09951-7

Query Match 100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13
13
1 TTPAYRPPNAPIL 13
Db

RESULT 13
US-09-100-409A-45
; Sequence 45, Application US/09100409A
; Patent No. 6090388
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
; TITLE OF INVENTION: IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100, 409A

FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1151-4154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-409A-45

Query Match 100.0%; Score 74; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 14
PCT-US95-13841-13
Sequence 13, Application PC/TUS9513841
GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Wallfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IGF Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13841
FILING DATE: 25-OCT-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/328,519
FILING DATE: 25-OCT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4117
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-13841-13

Query Match 100.0%; Score 74; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00036;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 9 TPPAYRPPNAPIL 21

RESULT 15
US-08-464-496-20
Sequence 20, Application US/08464496
Patent No. 6322789
GENERAL INFORMATION:
APPLICANT: EpiMune, Inc.
APPLICANT: Vitiello, Maria
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPITOPES
FILE REFERENCE: 39963-20001.13
CURRENT APPLICATION NUMBER: US/08/464,496
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 07/935,811
PRIOR FILING DATE: 1992-08-26
PRIOR APPLICATION NUMBER: 07/874,491
PRIOR FILING DATE: 1992-04-27
PRIOR APPLICATION NUMBER: 07/827,682
PRIOR FILING DATE: 1992-01-29
PRIOR APPLICATION NUMBER: 07/749,568
PRIOR FILING DATE: 1991-08-26
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T helper epitope HBC 128-140
US-08-464-496-20

Query Match 100.0%; Score 74; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

Search completed: December 14, 2004, 16:43:00
Job time : 8.775 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:38:07 ; Search time 32.5 Seconds

(without alignments)
142.871 Million cell updates/sec

Title: US-09-055-744A-10

Sequence: 1 TTPAYRPPNAPIL 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	74	100.0	13 9 US-09-055-744-10	Sequence 10, Appl
2	74	100.0	13 9 US-09-839-447A-86	Sequence 86, Appl
3	74	100.0	13 10 US-09-277-074-9	Sequence 9, Appl
4	74	100.0	13 10 US-09-277-064-9	Sequence 9, Appl
5	74	100.0	13 11 US-09-788-110A-4	Sequence 4, Appl
6	74	100.0	13 13 US-10-106-487-22	Sequence 22, Appl
7	74	100.0	13 14 US-10-128-711-113	Sequence 113, Appl
8	74	100.0	13 14 US-10-116-118-30	Sequence 30, Appl
9	74	100.0	13 14 US-10-371-525-49	Sequence 49, Appl
10	74	100.0	13 14 US-10-371-069-49	Sequence 49, Appl
11	74	100.0	13 14 US-10-371-645-49	Sequence 49, Appl
12	74	100.0	13 14 US-10-371-260-49	Sequence 49, Appl
13	74	100.0	13 14 US-10-372-735-55	Sequence 55, Appl

14 74 100.0 13 14 US-10-369-060A-86 Sequence 86, Appl
15 74 100.0 13 15 US-10-388-337-22 Sequence 22, Appl
16 74 100.0 13 15 US-10-608-541-50 Sequence 50, Appl
17 74 100.0 13 15 US-10-182-252A-1374 Sequence 1374, Ap
18 74 100.0 13 15 US-10-333-430-63 Sequence 63, Appl
19 74 100.0 13 16 US-10-808-681-5 Sequence 5, Appl
20 74 100.0 14 14 US-10-371-525-124 Sequence 124, App
21 74 100.0 14 14 US-10-371-069-124 Sequence 124, App
22 74 100.0 14 14 US-10-371-645-124 Sequence 124, App
23 74 100.0 14 14 US-10-371-260-124 Sequence 124, App
24 74 100.0 16 14 US-10-106-876-3 Sequence 3, Appl
25 74 100.0 18 14 US-10-106-876-10 Sequence 107, App
26 74 100.0 20 9 US-09-839-447A-107 Sequence 107, App
27 74 100.0 20 14 US-10-369-060A-107 Sequence 43, Appl
28 74 100.0 21 8 US-08-785-997-43 Sequence 43, Appl
29 74 100.0 21 10 US-09-387-340-43 Sequence 43, Appl
30 74 100.0 21 10 US-09-386-591-43 Sequence 114, Appl
31 74 100.0 23 14 US-10-128-711-114 Sequence 114, Appl
32 74 100.0 26 14 US-10-128-711-115 Sequence 115, Appl
33 74 100.0 80 14 US-10-371-069-22 Sequence 22, Appl
34 74 100.0 80 14 US-10-371-069-22 Sequence 22, Appl
35 74 100.0 80 14 US-10-371-645-22 Sequence 22, Appl
36 74 100.0 80 14 US-10-371-260-22 Sequence 22, Appl
37 74 100.0 118 14 US-10-371-525-8 Sequence 8, Appl
38 74 100.0 118 14 US-10-371-525-8 Sequence 8, Appl
39 74 100.0 118 14 US-10-371-645-8 Sequence 8, Appl
40 74 100.0 119 14 US-10-371-525-10 Sequence 10, Appl
41 74 100.0 119 14 US-10-371-069-10 Sequence 10, Appl
42 74 100.0 119 14 US-10-371-645-10 Sequence 10, Appl
43 74 100.0 119 14 US-10-371-260-10 Sequence 10, Appl
44 74 100.0 119 14 US-10-371-260-10 Sequence 10, Appl
45 74 100.0 136 14 US-10-371-525-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-055-744-10

Sequence 10, Application US/09055744

Publication No. US20010019714A1

GENERAL INFORMATION:

APPLICANT: Sia, Charles

APPLICANT: Chong, Pele

APPLICANT: Klein, Michel

TITLE OF INVENTION: HIV-SPECIFIC CYTOTOXIC T-CELL RESPONSES

FILE REFERENCE: 1038-746

CURRENT APPLICATION NUMBER: US/09/055, 744

CURRENT FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 13

TYPE: PRT

ORGANISM: Human immunodeficiency virus type 1

US-09-055-744-10

Query Match 100.0%; Score 74; DB 9; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTPAYRPPNAPIL 13

Db 1 TTPAYRPPNAPIL 13

RESULT 2

US-09-839-447A-86

Sequence 86, Application US/09839447A

Patent No. US20020058247A1

GENERAL INFORMATION:

APPLICANT: Salberg, Matci

TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE

```

; TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
; FILE REFERENCE: TRIPE.020CPI
; CURRENT APPLICATION NUMBER: US/09/839,447A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/555605
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 86
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-09-839-447A-86

Query Match      100.0%; Score 74; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 3
US-09-277-074-9
; Sequence 9, Application US/09277074
; Publication No. US20030022820A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21555
; CURRENT APPLICATION NUMBER: US/09/277,074
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-074-9

Query Match      100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 4
US-09-277-064-9
; Sequence 9, Application US/09277064
; Publication No. US20030064916A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Linda A.
; TITLE OF INVENTION: IN VIVO ACTIVATION OF TUMOR-SPECIFIC CYTOTOXIC T CELLS
; FILE REFERENCE: SCR21525
; CURRENT APPLICATION NUMBER: US/09/277,064
; CURRENT FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 08/355,558
; PRIOR FILING DATE: 1994-12-14
; PRIOR APPLICATION NUMBER: PCT/US95/16415
; PRIOR FILING DATE: 1995-12-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
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; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-277-064-9

Query Match      100.0%; Score 74; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 5
US-09-788-110A-4
; Sequence 4, Application US/09788110A
; Publication No. US20040086518A1
; GENERAL INFORMATION:
; APPLICANT: Zanetti, Maurizio
; TITLE OF INVENTION: A Universal Vaccine and Method for Treating Cancer Employing
; FILE REFERENCE: UCSD-07017
; CURRENT APPLICATION NUMBER: US/09/788,110A
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-110A-4

Query Match      100.0%; Score 74; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTPAYRPPNAPIL 13
Db      1 TTPAYRPPNAPIL 13

RESULT 6
US-10-106-487-22
; Sequence 22, Application US/10106487
; Publication No. US20020164721A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LEMONNIER, FRANCOIS
; APPLICANT: LANGLAD-DEMOYEN, PIERRE
; APPLICANT: MICHEL, MARIE-LOUISE
; TITLE OF INVENTION: DESIGN OF A POLYPEPTIDIC CONSTRUCT FOR THE INDUCTION
; TITLE OF INVENTION: OF
; TITLE OF INVENTION: HLA-A2.1 RESTRICTED HIV 1 SPECIFIC CTL RESPONSES USING
; FILE REFERENCE: 03495.0196 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/106,487
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/675,673
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/158,356
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-106-487-22

Query Match      100.0%; Score 74; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 7

US-10-128-711-113
Sequence 113, Application US/10128711
Publication No. US2003009634A1
GENERAL INFORMATION:
APPLICANT: VITTELO, Maria A.
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELLS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 14137-26-4
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-128-711-113

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

RESULT 8

US-10-116-118-30
Sequence 30, Application US/10116118
Publication No. US20030143672A1
GENERAL INFORMATION:
APPLICANT: Tangri, Shabnam
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn
APPLICANT: Fikes, John D.
TITLE OF INVENTION: Heterocyclic Analogs and Related Methods
FILE REFERENCE: 2060.0090003
CURRENT APPLICATION NUMBER: US/10/116,118
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/166,529
PRIOR FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: US 60/239,008
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In version 3.1
SEQ ID NO 30
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: (HBV core)
US-10-116-118-30
Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

US-10-371-525-49
Sequence 49, Application US/10371525
Publication No. US20030203869A1
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epiimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/10/371,525
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/311,784
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-525-49
Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
Db 1 TPPAYRPPNAPIL 13

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RESULT 10
US-10-371-069-49
; Sequence 49, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-069-49

Query Match          100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPAVRRPNAPIL 13
Db      1 TPAVRRPNAPIL 13

RESULT 11
US-10-371-645-49
; Sequence 49, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT FILING DATE: 2003-06-20
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-645-49

Query Match          100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPAVRRPNAPIL 13
Db      1 TPAVRRPNAPIL 13

RESULT 12
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49

Query Match          100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPAVRRPNAPIL 13
Db      1 TPAVRRPNAPIL 13

RESULT 13
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Salibery, Matci
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
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US-10-371-645-49

Query Match          100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPAVRRPNAPIL 13
Db      1 TPAVRRPNAPIL 13

RESULT 12
US-10-371-260-49
; Sequence 49, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: residues 128-141 of HBV core antigen (HBVcore 128)
US-10-371-260-49

Query Match          100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TPAVRRPNAPIL 13
Db      1 TPAVRRPNAPIL 13

RESULT 13
US-10-372-735-55
; Sequence 55, Application US/10372735
; Publication No. US20030225251A1
; GENERAL INFORMATION:
; APPLICANT: Salibery, Matci
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; FILE REFERENCE: TRIPEP.7AUC4CP1
; CURRENT FILING DATE: 2003-02-21
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 08/737,085
; PRIOR FILING DATE: 1996-12-27
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PRIOR APPLICATION NUMBER: PCT/SE95/00468
PRIOR FILING DATE: 1995-04-27
PRIOR APPLICATION NUMBER: 09/664,945
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/664,025
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: PCT/IB01/02327
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 10/153,271
PRIOR FILING DATE: 2002-05-21
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 199
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 55
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Synthesized Peptides
US-10-372-735-55

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. NO. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 14
US-10-369-060A-86
Sequence 86, Application US/10369060A
Publication No. US20030235815A1
GENERAL INFORMATION:
APPLICANT: Saliberg, Matci
TITLE OF INVENTION: SYNTHETIC PEPTIDES THAT BIND TO THE
TITLE OF INVENTION: HEPATITIS B VIRUS CORE AND E ANTIGENS
FILE REFERENCE: TRIPEP 020CPIC1
CURRENT APPLICATION NUMBER: US/10/369,060A
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 09/839,447
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/556,605
PRIOR FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 111
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 86
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Mus musculus
US-10-369-060A-86

Query Match 100.0%; Score 74; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. NO. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

RESULT 15
US-10-388-337-22
Sequence 22, Application US/10388337
Publication No. US20040018208A1
GENERAL INFORMATION:
APPLICANT: FIRAT, Huseyin
APPLICANT: LEMONNIER, Francois
APPLICANT: LANGLADE-DEMOYEN, Pierre
APPLICANT: MICHEL, Marie-Louise

APPLICANT: SUHRBIER, Andreas A
TITLE OF INVENTION: HYBRID OR CHIMERIC POLYNUCLEOTIDES, PROTEINS, AND
TITLE OF INVENTION: COMPOSITIONS COMPRISING HEPATITIS B VIRUS SEQUENCES
FILE REFERENCE: 03495,0198 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/388,337
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: US/09/671,198B
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/156,945
PRIOR FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 13
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-388-337-22

Query Match 100.0%; Score 74; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. NO. 0.0018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPPAYRPPNAPIL 13
DB 1 TPPAYRPPNAPIL 13

Search completed: December 14, 2004, 16:51:40
Job time : 33.5 secs

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